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CC The present sequence represents a monocyte mature differentiation
 CC factor which induces the state of macrophages for long periods
 CC in liquid culture. WMPF can be used as anti-cancer agent, an immune
 CC activator and to treat infectious diseases.

XX Sequence 381 AA:

Query Match 100.0%; Score 2115; DB 18; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5,1e-154;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSRRARALALVTLHLTRFLALSTCPAACHCPLAKACAGVLYRGGCCGVCAQL 60
 1 MSSRRARALALVTLHLTRFLALSTCPAACHCPLAKACAGVLYRGGCCGVCAQL 60
 61 NECCSKTPCHPTKGLGECNGASSALAKGICRAOSEGRCEYSRIYONCESFPNCKHQ 120
 61 NECCSKTPCHPTKGLGECNGASSALAKGICRAOSEGRCEYSRIYONCESFPNCKHQ 120
 61 NECCSKTPCHPTKGLGECNGASSALAKGICRAOSEGRCEYSRIYONCESFPNCKHQ 120
 121 CTCIGAVGCIPLCPQELSLPMLCAGCPRLVYKYGQCCFEMWCDEDSIKDPMEQGLLG 180
 121 CTCIGAVGCIPLCPQELSLPMLCAGCPRLVYKYGQCCFEMWCDEDSIKDPMEQGLLG 180
 121 CTCIGAVGCIPLCPQELSLPMLCAGCPRLVYKYGQCCFEMWCDEDSIKDPMEQGLLG 180
 181 KEIGDASVEVLTNNELIYVKGSSSLKRLPYGMEPRLLYNPLQSKCIYVTTSSQCS 240
 181 KEIGDASVEVLTNNELIYVKGSSSLKRLPYGMEPRLLYNPLQSKCIYVTTSSQCS 240
 181 KEIGDASVEVLTNNELIYVKGSSSLKRLPYGMEPRLLYNPLQSKCIYVTTSSQCS 240
 241 KTCGGTGSTRTVNDNPECRILYERIRICEVRPCGQPYVSSLKKGKCSRTKSPPYRFTY 300
 241 KTCGGTGSTRTVNDNPECRILYERIRICEVRPCGQPYVSSLKKGKCSRTKSPPYRFTY 300
 301 AGCLSVKKYRRCYSGCVDRCCCPQLRTVYKMRFCEDGETFSKNVAMIOSCKMNCIP 360
 301 AGCLSVKKYRRCYSGCVDRCCCPQLRTVYKMRFCEDGETFSKNVAMIOSCKMNCIP 360
 361 HANEAAFPFYRLFNDIHRFD 381
 361 HANEAAFPFYRLFNDIHRFD 381

DB

RESULT 2
 AAB90773
 ID AAB90773 standard; Protein: 381 AA.

XX AAB90773:

15-JUN-2001 (first entry)

Human shear stress-response protein SRQ ID NO: 46.

Human shear stress-response protein; vascular disease;
 arteriosclerosis.

XX Homo sapiens.

XX WO200125427-A1.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-JP06840.

XX 01-OCT-1999; 99JP-0280976.

XX (KYO) KYOMA HAKKO KOSYO KK.

XX (NOJL) NOJIMA H.

XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;

XX Kuga T, Sekine Y, Nakamura Y, Sugano S;

XX WPI: 2001-36308/27.

XX N-ESDB; AAB902956.

XX DNA sequences, proteins encoded by them and antibodies against them

PT useful in diagnosis and treatment of vascular disease caused by
 PT arteriosclerosis -
 PS Claim 60; Page 345-346; 678pp; Japanese.

CC The present invention provides the protein and coding sequences of a
 CC number of human shear stress response proteins. These are useful in the
 CC diagnosis, treatment and screening of vascular diseases caused by
 CC arteriosclerosis, including heart failure, post-PTCA restenosis and
 CC hypertension.

XX Sequence 381 AA:

Query Match 100.0%; Score 2115; DB 22; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5,1e-154;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSRRARALALVTLHLTRFLALSTCPAACHCPLAKACAGVLYRGGCCGVCAQL 60
 1 MSSRRARALALVTLHLTRFLALSTCPAACHCPLAKACAGVLYRGGCCGVCAQL 60
 61 NECCSKTPCHPTKGLGECNGASSALAKGICRAOSEGRCEYSRIYONCESFPNCKHQ 120
 61 NECCSKTPCHPTKGLGECNGASSALAKGICRAOSEGRCEYSRIYONCESFPNCKHQ 120
 61 NECCSKTPCHPTKGLGECNGASSALAKGICRAOSEGRCEYSRIYONCESFPNCKHQ 120
 121 CTCIGAVGCIPLCPQELSLPMLCAGCPRLVYKYGQCCFEMWCDEDSIKDPMEQGLLG 180
 121 CTCIGAVGCIPLCPQELSLPMLCAGCPRLVYKYGQCCFEMWCDEDSIKDPMEQGLLG 180
 121 CTCIGAVGCIPLCPQELSLPMLCAGCPRLVYKYGQCCFEMWCDEDSIKDPMEQGLLG 180
 181 KEIGDASVEVLTNNELIYVKGSSSLKRLPYGMEPRLLYNPLQSKCIYVTTSSQCS 240
 181 KEIGDASVEVLTNNELIYVKGSSSLKRLPYGMEPRLLYNPLQSKCIYVTTSSQCS 240
 181 KEIGDASVEVLTNNELIYVKGSSSLKRLPYGMEPRLLYNPLQSKCIYVTTSSQCS 240
 241 KTCGGTGSTRTVNDNPECRILYERIRICEVRPCGQPYVSSLKKGKCSRTKSPPYRFTY 300
 241 KTCGGTGSTRTVNDNPECRILYERIRICEVRPCGQPYVSSLKKGKCSRTKSPPYRFTY 300
 301 AGCLSVKKYRRCYSGCVDRCCCPQLRTVYKMRFCEDGETFSKNVAMIOSCKMNCIP 360
 301 AGCLSVKKYRRCYSGCVDRCCCPQLRTVYKMRFCEDGETFSKNVAMIOSCKMNCIP 360
 361 HANEAAFPFYRLFNDIHRFD 381
 361 HANEAAFPFYRLFNDIHRFD 381

DB

RESULT 3
 AAB90761
 ID AAB90761 standard; Protein: 381 AA.

XX AAB90761:

30-JUL-2002 (first entry)

Human Cyf61 protein.

Human; uterine leiomyoma proliferation; uterine leiomyoma formation;
 Cyf61; cytotatic.

XX Homo sapiens.

XX WO200226193-A2.

XX 04-APR-2002.

XX 28-SEP-2001; 2001WO-US30783.

XX 29-SEP-2000; 2000US-236887P.

XX (AMIP) AMERICAN HOME PROD CORP.

XX Zhang Z, Sampath D, Zhu Y, Wincker R;

DR WPI; 2002-383245/41
DR N-PSDB; ABK48899.

PT Preventing uterine leiomyoma formation or inhibiting proliferation of
PT uterine leiomyoma in subject, comprises modulating or increasing the
PT level of Cyt61 in leiomyoma tissue -

PS Disclosure; Fig 6; 92pp; English.

The present invention relates to a method of inhibiting proliferation of uterine leiomyoma or preventing uterine leiomyoma formation. The method comprises increasing the level of Cyt1 in leiomyoma tissue. The invention also describes compounds and compositions that stimulate the expression of the Cyt1 gene and compounds that increase Cyt1 activity. The compounds that increase Cyt1 gene expression are useful for preventing uterine leiomyoma formation or inhibition of uterine leiomyoma in a subject. The method is particularly useful for treating or preventing uterine leiomyoma formation, or inhibiting proliferation of uterine leiomyoma in a subject. The present sequences represent human Cyt1.

Note: The present sequence shown in Fig 6 is not shown in the correct page 8/10 of the figures and the rest of the sequence is shown on page 6/10 of the figures.

SQ Sequence 381 AA;

Query Match	100.00;	Score 2115;	DB 23;	Length 381;
-------------	---------	-------------	--------	-------------

```
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY 1 MSSRIARALAVTLLHLTRIALSTCPACHCPLLEAPKCAPGVGLVRDGGCCCKVC AKOL 60

[illegible]

RESULT 4

AC AAE18107

DT 07-MAY-2002 (first entry

DE Human connective tissue growth factor-2 (CTGF-2)

KW Human; angiogenesis; connective tissue growth factor-2; CTGF-2; tumour
 KW ischaemia; restenosis; tissue repair; wound healing; congenital defect
 KW cardiovascular disease; atherosclerosis; heart failure; angina; trauma

xx
xx
Homo sapiens.
AS

KW gene therapy.

KM burn; osteoporosis; periodontal disease; liver failure; tranquilizer

RN vulnary; cosmetic plastic surgery; vasotropic; hepatotropic; ulcer;

FM Key

Location/Qualifiers

```

Region 33,41
FI "Tumorigenic antineoplastic"
CPT /note=

```

Region	47.51
FT	

FT	Region	59.75
----	--------	-------

Region	91..119
FT	

Region	FP	EP	/note= "Immunogenic epitope"
145	150		

/note= "Immunogenic epitope"

```

FT
/note= "Immunogenic epitope"

```

FT	negLOU	202.1.200	/note- "Immunogenic epitope"
F1	negLOU	202.1.200	/note- "Immunogenic epitope"

Region	223.228
Region	223.228

FT	Region	239.244
----	--------	---------

FT	Region	250..257
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
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15	15	15
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19	19	19
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22	22	22
23	23	23
24	24	24
25	25	25
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27	27	27
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32	32	32
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34	34	34
35	35	35
36	36	36
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38	38	38
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42	42	42
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84	84	84
85	85	85
86	86	86
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91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

Region	Immunogenic epitope	FT
279-296		

Ref	Region	/note= "Immunogenic epitope"
207	314	

/note= "Immunogenic epitope"

PN WO200204480-A2

PD 17-JAN-2002.

11-JUL-2001; 2001WO-US21799

11-JUL-2000: 2000US-217402F

PR 18-MAY-2001; 2001US-291642F

PA (HUMA-) HUMAN GENOME SCI INC.

[illegible]

PL H, Adams MD, Calenda V, Faccacciolli V
XX

DR WPI; 2002-171698/22

XX

or restenosis or is treated for limb revascularization, by

PS Example 1; Fig 1; 131pp; English

The present invention relates to a method for stimulating angiogenesis in a mammal. The method comprises administering a polynucleotide encoding connective tissue growth factor-2 (CTGF-2) or an active fragment or its derivative. The method is useful for stimulating angiogenesis in a mamma preferably human having ischaemia or restenosis or is treated for limb revascularisation which is leg or arm. The invention is useful for inhibiting tumour growth, where angiogenesis is utilised for enhancing blood supply to the tumour. The invention is also useful for enhancing fixation and stabilisation of tissue implants and enhancing wound healing, hence is useful for treating cardiovascular disease e.g. atherosclerosis, reperfusion injury such as heart failure, angina, CC ischemia; and is also used to differentiate, proliferate and attract cells leading to regeneration of tissues which is utilised to repair

CC Replace or protect tissue damaged by congenital defects, trauma (burns,
 CC ulcer, etc), age, disease (e.g. osteoporosis, periodontal disease,
 CC liver failure), surgery including cosmetic plastic surgery. The present
 CC sequence is human Cyt61. Cyt61-2 gene is useful in gene therapy.

50 Sequence 381 AA;

Query Match 100.0%; Score 2115; DB 23; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5,1e-154;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MSSRIARALATVTLTLHTLSTCPMACGCELPKACAGVGLVDGCGCCVCAKOL 60
 DB 1 MSSRIARALATVTLTLHTLSTCPMACGCELPKACAGVGLVDGCGCCVCAKOL 60
 0Y 61 NECSKTOPCHRTKGLECNAGSSTLAKGICRAOSEGRCEYSRTYONGSEFOPKCHQ 120
 DB 61 NECSKTOPCHRTKGLECNAGSSTLAKGICRAOSEGRCEYSRTYONGSEFOPKCHQ 120
 0Y 121 CTCIDGAVGCIPLCQDELSTPLACGPNRLVYTGQCEBNVCDDESIKDPMEODGILG 180
 DB 121 CTCIDGAVGCIPLCQDELSTPLACGPNRLVYTGQCEBNVCDDESIKDPMEODGILG 180
 0Y 181 KEJGFDASVEELTRNNELIAVKGSSSLKRLPVEGMEERLYLNPQGNKCIYOTISWCS 240
 DB 181 KEJGFDASVEELTRNNELIAVKGSSSLKRLPVEGMEERLYLNPQGNKCIYOTISWCS 240
 0Y 241 KTCGIGSTRYNDNPECLRYEIRLCEVRGCGPYSSLKAKKCSKTKSPPEPRY 300
 DB 241 KTCGIGSTRYNDNPECLRYEIRLCEVRGCGPYSSLKAKKCSKTKSPPEPRY 300
 0Y 301 AGCLSVKTRKTCGSCYDRCCTPOLRTYKMRKREDEGETSKNWMIOCKCNVMP 360
 DB 301 AGCLSVKTRKTCGSCYDRCCTPOLRTYKMRKREDEGETSKNWMIOCKCNVMP 360
 0Y 361 HANEAAPEPYRLFNIDHFRD 381
 DB 361 HANEAAPEPYRLFNIDHFRD 381

RESULT 5
 ABB05438
 ID ABB05438 standard; Protein: 381 AA.
 AC ABB05438;
 XX 15-APR-2002 (first entry)
 DT Human Cyt61 protein SEQ ID NO.2.
 XX
 XX Human; Cyt61: breast cancer; sex steroid receptor; cytosolic; promoter;
 KW sex steroid response element; cysteine rich heparin binding protein;
 KW cell proliferation; heparin binding epidermal growth factor;
 XX epidermal growth factor; basic fibroblastic growth factor.
 XX Homo sapiens.
 XX
 XX WO200198359-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 21-JUN-2001; 2001WO-0519823.
 XX
 XX 21-JUN-2000; 2000US-23182P.
 XX
 XX 16-MAY-2001; 2001US-291510P.
 XX
 XX (AMHP) AMERICAN HOME PROD CORP.
 XX
 XX Sampath D, Zhang Z, Wloneker R;
 XX
 XX WPI: 2002-147796/19
 XX
 XX N-PSDB: ABA93127, ABA93130.
 XX

PT Regulation of Cyt61 expression and activity for preventing and
 PT inhibiting breast cancer comprises use of a Cyt61 neutralizing
 PT antibody, an anti-sense oligonucleotide and an antibody which
 XX
 XX Claim 6; Fig 1; 86pp; English.

CC The present invention describes a method for the prevention or inhibition
 CC of breast cancer cell proliferation. The method comprises administration
 CC of a compound that inhibits the interaction of a sex steroid receptor
 CC with a sex steroid response element of the Cyt61 (cysteine rich heparin-
 CC binding protein) promoter. Cyt61 has cytosolic activity. An antibody (1)
 CC that binds to the Cyt61 protein inhibits the interaction of Cyt61 with
 CC cell proliferation by blocking sex steroid induced and growth factor
 CC induced synthesis of Cyt61 DNA, where the growth factor is epidermal,
 CC heparin binding epidermal or basic fibroblastic growth factor. (1) can be
 CC used to diagnose or stage breast cancer where the level of Cyt61 in a
 CC normal cell, an increase in the level of Cyt61 compared to the level in
 CC Cyt61 binding determined by exposing the tissues to (1), and an increase
 CC in the level of bound antibody by the presence of breast cancer cell as compared
 CC to the normal tissue indicates the presence of breast cancer. The present
 CC sequence represents the human Cyt61 protein, which is used in the
 CC exemplification of the present invention.

50 Sequence 381 AA;

Query Match 100.0%; Score 2115; DB 23; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5,1e-154;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MSSRIARALATVTLTLHTLSTCPMACGCELPKACAGVGLVDGCGCCVCAKOL 60
 DB 1 MSSRIARALATVTLTLHTLSTCPMACGCELPKACAGVGLVDGCGCCVCAKOL 60
 0Y 61 NECSKTOPCHRTKGLECNAGSSTLAKGICRAOSEGRCEYSRTYONGSEFOPKCHQ 120
 DB 61 NECSKTOPCHRTKGLECNAGSSTLAKGICRAOSEGRCEYSRTYONGSEFOPKCHQ 120
 0Y 121 CTCIDGAVGCIPLCQDELSTPLACGPNRLVYTGQCEBNVCDDESIKDPMEODGILG 180
 DB 121 CTCIDGAVGCIPLCQDELSTPLACGPNRLVYTGQCEBNVCDDESIKDPMEODGILG 180
 0Y 181 KEJGFDASVEELTRNNELIAVKGSSSLKRLPVEGMEERLYLNPQGNKCIYOTISWCS 240
 DB 181 KEJGFDASVEELTRNNELIAVKGSSSLKRLPVEGMEERLYLNPQGNKCIYOTISWCS 240
 0Y 241 KTCGIGSTRYNDNPECLRYEIRLCEVRGCGPYSSLKAKKCSKTKSPPEPRY 300
 DB 241 KTCGIGSTRYNDNPECLRYEIRLCEVRGCGPYSSLKAKKCSKTKSPPEPRY 300
 0Y 301 AGCLSVKTRKTCGSCYDRCCTPOLRTYKMRKREDEGETSKNWMIOCKCNVMP 360
 DB 301 AGCLSVKTRKTCGSCYDRCCTPOLRTYKMRKREDEGETSKNWMIOCKCNVMP 360
 0Y 361 HANEAAPEPYRLFNIDHFRD 381
 DB 361 HANEAAPEPYRLFNIDHFRD 381

RESULT 6

AAB43987
 ID AAB43987 standard; Protein: 455 AA.

XX AAB43987;
 XX

XX 08-FEB-2001 (first entry)
 XX

XX Human cancer associated protein sequence SEQ ID NO:1432.
 XX

XX Human; cancer associated gene; cancer antigen; immunogen; cancer;
 KW diagnosis; cytosolic; proliferative; vulvar; immunomodulator;
 XX antidiabetic; antilastmotic; antineumatic; antilarthritic; antiviral;
 KW


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OY 1 MSSRIARALALVYTLHLTRILALSTCPAACHCEPLAKKARGVGLVBDGCGCKVCANOL 60
DB 1 MSSRIARALALVYTLHLTRILALSTCPAACHCEPLAKKARGVGLVBDGCGCKVCANOL 60
OY 61 NECSKTOPCDHRTKGLCECNASSSTALGICRAOSEGRRCYSRITONGESPQPCOH 120
DB 61 NECSKTOPCDHRTKGLCECNASSSTALGICRAOSEGRRCYSRITONGESPQPCOH 120
OY 121 CTCIDGAVGCIPLCPQELSLPILGICPNRLVLYVGGCCCEWVCDEDSIKDPEBDODGLD 180
DB 121 CTCIDGAVGCIPLCPQELSLPILGICPNRLVLYVGGCCCEWVCDEDSIKDPEBDODGLD 180
OY 181 KEIGDASEVELTRNNELIANGKSKRLRPLVFGMERILYVLOGOKIVOTTSSQGS 240
DB 181 KEIGDASEVELTRNNELIANGKSKRLRPLVFGMERILYVLOGOKIVOTTSSQGS 240
OY 241 KTCGTGISTRVYNDNPECRIVETRICEVRCGCPVYSLLKKKKSKTKSKTPPEVRY 300
DB 241 KTCGTGISTRVYNDNPECRIVETRICEVRCGCPVYSLLKKKKSKTKSKTPPEVRY 300
OY 301 AGCLSVKRYRKYGSCVGDRCCTPOLRTFVYKMRFCEDGCTPSKANNWIOSCKYVNC 360
DB 301 AGCLSVKRYRKYGSCVGDRCCTPOLRTFVYKMRFCEDGCTPSKANNWIOSCKYVNC 360
OY 361 HANEAPPPYRLNDFNDRFD 381
DB 361 HANEAPPPYRLNDFNDRFD 381

RESULT 8
AAE05921 standard; Protein: 381 AA.
AAE05921:
24-SEP-2001 (first entry)

Human cysteine-rich protein (Cyf61).
Human cysteine-rich protein (Cyf61).
Cysteine-rich protein: Cyf61; extracellular matrix signalling molecule;
cyf61; secreted protein; fisp2; connective tissue growth factor;
cyf61; secreted protein; fisp2; connective tissue growth factor;
angiogenesis; wound healing; integrin receptor; atherosclerosis; tumour;
heart disease; fibrosis; gene therapy; human.
Homo sapiens.
Key:
Region 163..329
/notes= "Cysteine free region"
Domain 212..281
/notes= "Domain III"
Domain 282..381
/notes= "Domain IV"

MO200155210-42.
02-AUG-2001.
31-JAN-2001: 2001WO-US03267.
31-JAN-2000: 2000US-0495448.
15-MAY-2000: 2000US-0204384.
06-OCT-2000: 2000US-0238705.
(MUNF-) MUNIN CORP.
Lau LF, Yeung C, Greenspan JA:
WPI: 2001-465561/50.
N-PSDB: AAD1121.
Novel human cysteine-rich protein 61 (Cyf61) fragment useful in methods

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PT for screening for modulators of cell adhesion, fibroblast cell
PT proliferation, angiogenesis and cell migration.
XX Claim 30: Page 171-172; 16pp; English.
XX The invention relates to extracellular matrix (ECM) signalling
XX molecules involved in cellular response to growth factors. More
XX particularly the invention is directed to cysteine-rich protein
XX (Cyf61), and Cyf61-related proteins such as fibroblast secreted
XX protein (fisp2) and connective tissue growth factor (CTGF) and
XX secreted protein encoding cysteine-rich proteins (Cyf61) and
XX of the invention are useful in methods for screening
XX modulators of cell adhesion, cell migration, fibroblast cell
XX proliferation, angiogenesis, wound healing and Cyf61-integrin
XX receptor interaction. Modulator of Cyf61-integrin alphaVbeta3
XX interaction is used for the preparation of a treatment for the
XX treatment of atherosclerosis, heart disease, tumour metastasis,
XX angiogenesis, aberrant granulation tissue development, aberrant
XX fibroblast growth and wounds. Polynucleotides of the invention
XX are useful in gene therapy. The present sequence is human Cyf61
XX protein.
XX Sequence 381 AA:
XX
XX Query Match 99.6%; Score 2106; DB 22; Length 381;
XX Best Local Similarity 99.5%; Pred No. 2.5e-153;
XX Matches 379; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 MSSRIARALALVYTLHLTRILALSTCPAACHCEPLAKKARGVGLVBDGCGCKVCANOL 60
DB 1 MSSRIARALALVYTLHLTRILALSTCPAACHCEPLAKKARGVGLVBDGCGCKVCANOL 60
OY 61 NECSKTOPCDHRTKGLCECNASSSTALGICRAOSEGRRCYSRITONGESPQPCOH 120
DB 61 NECSKTOPCDHRTKGLCECNASSSTALGICRAOSEGRRCYSRITONGESPQPCOH 120
OY 121 CTCIDGAVGCIPLCPQELSLPILGICPNRLVLYVGGCCCEWVCDEDSIKDPEBDODGLD 180
DB 121 CTCIDGAVGCIPLCPQELSLPILGICPNRLVLYVGGCCCEWVCDEDSIKDPEBDODGLD 180
OY 181 KEIGDASEVELTRNNELIANGKSKRLRPLVFGMERILYVLOGOKIVOTTSSQGS 240
DB 181 KEIGDASEVELTRNNELIANGKSKRLRPLVFGMERILYVLOGOKIVOTTSSQGS 240
OY 241 KTCGTGISTRVYNDNPECRIVETRICEVRCGCPVYSLLKKKKSKTKSKTPPEVRY 300
DB 241 KTCGTGISTRVYNDNPECRIVETRICEVRCGCPVYSLLKKKKSKTKSKTPPEVRY 300
OY 301 AGCLSVKRYRKYGSCVGDRCCTPOLRTFVYKMRFCEDGCTPSKANNWIOSCKYVNC 360
DB 301 AGCLSVKRYRKYGSCVGDRCCTPOLRTFVYKMRFCEDGCTPSKANNWIOSCKYVNC 360
OY 361 HANEAPPPYRLNDFNDRFD 381
DB 361 HANEAPPPYRLNDFNDRFD 381

RESULT 9
AB09202 standard; Protein: 374 AA.
AB09202:
08-JUL-2002 (first entry)
HCGF CNN family protein sequence SEQ ID NO:12.
Human; small GTP-like growth factor; SCGF; vulntraty; osteopontin;
KW gene therapy; muscle wasting disease; osteoporosis; wound healing;
XX tissue regeneration; angiogenesis.
XX

```


OS Unidentified.
 XX US2002049304-A1.
 XX 25-APR-2002.
 XX 14-MAY-2001. 2001US-0853625.
 PF 06-JUN-1995; 9505-0468847.
 PR 01-APR-1998; 9805-0053587.
 XX (HASTV) HASTINGS G A.
 XX (RDMK) ADAMS M D.
 PI Hastings CA. Adams MD.
 DR WPI: 2002-382150/41.
 XX Novel isolated polynucleotide sequence encoding a human small CCN-like
 PT growth factor, useful for treating muscle wasting disease, and
 XX osteoporosis -
 PS Disclosure: Fig 2A-D: 33pp: English.
 XX The present invention describes human small CCN-like growth factor
 CC (SCGF). SCGF has vulnerary and osteoplastic activities, and can be used
 CC in gene therapy. The SCGF polypeptides and polynucleotides can be used
 CC for treating muscle wasting diseases, and osteoporosis, and to stimulate
 CC bone growth. The SCGF polypeptides and polynucleotides can be used to
 CC stimulate proliferation of vascular smooth muscle cells and cell
 CC production. The present sequence represents a CNN family protein which
 CC is given in comparison with the human SCGF in the exemplification of the
 CC present invention.
 XX Sequence 374 AA:
 SQ
 Query Match 93.6%; Score 1980.5; DB 23; Length 374;
 Best Local Similarity 96.3%; Pred. No. 1e-143;
 Matches 360; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

AC AAR90919;
 DT 25-JUN-1996 (first entry)
 XX Connective tissue growth factor-2.
 DE CTGF-2: connective tissue growth factor-2; secreted protein;
 XX cartilaginous growth; skeletal; embryo; cell growth; morphogenesis;
 KW Insulin-like growth factor; fibroblast growth factor; Cyt61.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FH Peptide /label= signal-peptide
 FT Protein 25..375
 FT /label= mature.protein
 XX MO9601896-A.
 PN 25-JAN-1996.
 XX 12-JUL-1994; 94MO-US07736.
 PF 12-JUL-1994; 94MO-US07736.
 PR 12-JUL-1994; 94MO-US07736.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Adams MD, LA H;
 XX WPI: 1996-097626/10.
 DR N-PSDS: AAT12653.
 DR
 XX Connective tissue growth factor-2 and DNA encoding it - useful to
 PT enhance the repair of connective and support tissue, and to enhance
 PT wound healing
 XX Claim 1: Fig 1A-C: 46pp: English.
 PS
 XX Connective tissue growth factor-2 (CTGF-2) is encoded by a cDNA
 CC (AAT12653) isolated from a human foetal lung cDNA library. The CTGF
 CC polypeptides are structurally and functionally related to a family
 CC of growth factors which include the (transulin-like growth factor),
 CC (platelet-derived growth factor), and the (transforming growth factor).
 CC Factor CTGF-2 exhibits 89 percent identity and 93 percent similarity
 CC to Cyt61. Cyt61 is a growth factor-inducible immediate early gene
 CC initially identified in serum-stimulated mouse fibroblasts. It encodes
 CC a member of an emerging family of secreted proteins which are also a
 CC group of cysteine-rich proteins. This group of GFs are important for
 CC normal growth, differentiation, morphogenesis of the cartilaginous
 CC skeleton of an embryo and cell growth.
 CC
 XX Sequence 375 AA:
 SQ
 Query Match 93.6%; Score 1980.5; DB 17; Length 375;
 Best Local Similarity 96.3%; Pred. No. 1e-143;
 Matches 360; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

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GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 8, 2003, 12:26:17 ; Search time 40 Seconds

(without alignments) 915.680 Million cell updates/sec

Title: US-09-901-910-2

Perfect score: 2115

Sequence: 1 MSSRIANAALAVTLILHLTR.....ANCAAPFYRLFDHDKRND 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR-73:*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1938	91.6	379	A35669		gene Cyrl6 protein
2	1699	80.3	375	A41428		Cyrl-10 protein pre
3	956.5	45.2	348	A40578		beta IG-M2 protein
4	951	45.0	349	A40551		connective tissue
5	855.5	40.4	352	S20078		NOV protein - chlc
6	834.5	39.5	357	139068		gene nov protein
7	1713.2	8.3	1524	T24293		hypothetical prote
8	1379.2	8.2	1132	T24293		hypothetical prote
9	159	7.5	1700	S08167		B2Hnrl rln3 pr
10	156	7.4	1574	T13954		MG35 protein - ra
11	153	7.2	837	A42112		muslin-like peptid
12	152.5	7.2	1178	A39804		thomaspodn pre
13	152	7.2	5376	T42215		lamnin B1k chain
14	147.5	7.0	1170	A55612		hypothetical prote
15	145	6.9	601	D86713		notch4 - mouse
16	145	6.9	601	D86713		notch4 - mouse
17	144	6.8	1964	T09059		secreted lauche-r
18	142	6.7	1025	T42626		muslin - rat
19	141.5	6.7	1034	JC5598		hypothetical prote
20	141.5	6.7	1101	T16840		muslin 2 precursor
21	141.5	6.7	13288	T03099		muslin, submaxillar
22	141.1	6.7	3028	A43932		muslin 2 precursor
23	141.1	6.6	1042	A55534		muslin 5AC clone 1
24	139	6.6	1042	A55534		muslin 5AC clone 1
25	138	6.5	251	A55035		crystalline-rich pr
26	138	6.5	2437	T42612		notch protein homo
27	136	6.4	2531	S18188		tenascin-X - bovin
28	136	6.4	4135	T42629		tenascin-X - bovin
29	135	6.4	473	A56175		adhesive plaque pr

ALIGNMENTS

RESULT 1
A35669
gene Cyrl6 protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence-revision 18-Nov-1992 #text-change 05-Nov-1999
C:Accession: A35669; 148319; S16446
Mol Biol, Biol: 10:3660-3672; 1990, L.; Lau, L.F.
A:Title: Expression of cyrl6, a growth factor-inducible immediate-early gene.
A:Reference number: A35669; WUID:90287146; PMID:2355916
A:Accession: A35669
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-379 (CODE)
A:Notes: The authors translated the codon GAT for residue 337 as Gln
R1atkinic, B.V.; O'Brien, T.P.; Lau, L.F.
Nucleic Acids Res. 19, 3261-3267, 1991
A:Title: Promoter function and structure of the growth factor-inducible immediate ear
A:Reference number: 148319; WUID:91286203; PMID:2062642
A:Accession: 148319
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-379 (CODE)
A:Notes: The authors translated the codon GAT for residue 337 as Gln
A:Cross-references: EMBL:X56790; NID:950632; PIRN:CAA0109.1; PID:950633
A:Note: the authors did not translate the codon for residue 108
A:Note: the authors translated the codon GAT for residue 337 as Gln
C:Genes: CYR61
A:Antons: 213; 93/1; 206/1; 279/3
A:Notes: von Millebrand factor type C repeat homology <MWC>
F:99-166/Domain: von Millebrand factor type C repeat homology <MWC>
Query Match 91.6%; Score 1938; DB 2; Length 379;
Best Local Similarity 91.4%; Pred. No. 4.5e-135;
Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2;
1 MSSRIANAALAVTLILHLTRALSTGPAACHCLEAKCARGLVDRGGCCYKVAQL 60
1 MSSRFTLAVALVTLILHLTRALSTGPAACHCLEAKCARGLVDRGGCCYKVAQL 60
61 NECKSKFOCHRTGGLGECNFGASFTALGICRAOSBORCYSNRIVYONCESFOPNCKHQ 120
61 NECKSKFOCHRTGGLGECNFGASFTALGICRAOSBORCYSNRIVYONCESFOPNCKHQ 120
121 CTCICGAVGCCIPCLCPQLSLPFLACNPRIVKYSGCCCEWVCDSDSIXDSDQDDL- 178
121 CTCICGAVGCCIPCLCPQLSLPFLACNPRIVKYSGCCCEWVCDSDSIXDSDQDDL- 178
181 KETGDSAEVELTRNNELIVAGKSSIKRLPVGVEPRILVNL--GGKCIIVPTSSSQ 238
179 --LSDASVEELTRNNELIVAGKSSIKRLPVGVEPRILVNLKOKCIIVPTSSSQ 236

Oy 239 CSKTCGTGISTRTVNDNPECLVKEERICVBPCCOPYSSLKAKKCKSKTKKSPPEVR 298
 Db 237 CSKCTGGTGSTRTVNDNPECLVKEERICVBPCCOPYSSLKAKKCKSKTKKSPPEVR 296
 Oy 299 TYAGCISVYKRYKRCGSCVGRCCCPOLRTFYVMKRFCEDEGFPSKNYMIQSCCKV 358
 Db 297 TYAGCISVYKRYKRCGSCVGRCCCPOLRTFYVMKRFCEDEGFPSKNYMIQSCCKV 356
 Oy 359 CPHANEALAPFYRLFMIDHKRD 381
 Db 357 CPHANEALAPFYRLFMIDHKRD 379

RESULT 2

CDR-10 protein precursor - chicken
 C:Accession: A41428
 C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jul-2000
 R:Simmons, D.L.; Levy, D.B.; Yarnool, Y.; Erikson, R.L.
 Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
 A:Title: Identification of a phorbol ester-repressible v-src-inducible gene.
 A:Reference number: A41428, MUID:89145206, PMID:2537491
 A:Accession: A41428
 A:Status: preliminary
 A:Description: Differential cloning and expression of fisp-12, a growth factor-inducible gene
 A:Molecule type: mRNA
 A:Residues: 1-375 <SNP>
 A:Cross-references: GB:M04496; NID:g211435; PIDN:AAA4861.1; PID:g211436

Query Match

Best Local Similarity 80.3%; Score 1699; DB 2; Length 375;
 Matches 512; Conservative 19; Mismatches 41; Indels 12; Gaps 7;

Oy 1 NSSRIKALAVLTLHLTRAL-STCPACACHPLE-ARKCAPGVGLVRGCGCKKVCYCK 59
 Db 1 MGSARAP-ALAAALILCLARALGSPKAVCCQCAAPACNPGVGLPVGCGCKVCYCK 59
 Oy 60 LNECSKTQPCDHTKGLCECNQASSTALCKICRMOSEGRCEYNSRTYONCESFPNCK 119
 Db 60 LNECSKTQPCDHTKGLCECNQASSTALCKICRMOSEGRCEYNSRTYONCESFPNCK 119
 Oy 120 OCTCIGAVGCIPLCPQELSLPMLGCPMPRLVKTGQCCCEWYCDDESIKDPMEDDGL 179
 Db 120 OCTCIGAVGCIPLCPQELSLPMLGCPMPRLVKTGQCCCEWYCDDESIKDPMEDDGL 177
 Oy 180 GRELGDSEVELTFNNELAVKSSSLKRLVEGNEP-RILYNLQOCCTVOTTSMS 237
 Db 178 SHELGDSEVELTFNNELAVKSSSLKRLVEGNEP-RILYNLQOCCTVOTTSMS 232
 Oy 238 OCSKTGCGISTRTVNDNPECLVKEERICVBPCCOPYSSLKAKKCKSKTKKSPPEVR 297
 Db 233 OCSKTGCGISTRTVNDNPECLVKEERICVBPCCOPYSSLKAKKCKSKTKKSPPEVR 292
 Oy 298 FTYAGCISVYKRYKRCGSCVGRCCCPOLRTFYVMKRFCEDEGFPSKNYMIQSCCKV 357
 Db 293 FTYAGCISVYKRYKRCGSCVGRCCCPOLRTFYVMKRFCEDEGFPSKNYMIQSCCKV 352
 Oy 358 NCPHANEALAPFYRLFMIDHKRD 381
 Db 353 NCPHANEALAPFYRLFMIDHKRD 375

RESULT 3

beta Ig-M2 protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 01-Dec-2000
 C:Accession: A40578
 R:Brunker, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.
 Dev. Cell Biol. 10, 293-300, 1991
 A:Title: Identification of a gene family regulated by transforming growth factor-beta.
 A:Reference number: A40578, MUID:91226937, PMID:2023537

A:Accession: A40578
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Cross-references: GB:M0261; NID:g201945; PIDN:AA77115.1; PID:g201946
 R:Bruck, R.P.; Macdonald-Bryvo, H.; Metcalf, M.G.; Bravo, R.
 Cell Growth Differ. 2, 225-233, 1991
 A:Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene
 A:Reference number: A53228, MUID:91363290, PMID:1888698
 A:Accession: A53228
 A:Status: preliminary
 A:Description: Differential cloning and expression of fisp-12, a growth factor-inducible gene
 A:Molecule type: mRNA
 A:Residues: 1-160, 162-348 <RFS>
 A:Cross-references: GB:M70641; NID:g93313; PIDN:AAA7627.1; PID:g93314
 A:Gene: fisp-12

Query Match 45.2%; Score 956.5; DB 2; Length 348;
 Best Local Similarity 46.3%; Score 961.5; DB 2; Length 348;
 Matches 179; Conservative 56; Mismatches 100; Indels 41; Gaps 8;

Oy 1 NSSRIKALAVLTLHLTRAL-STCPACACHPLE-ARKCAPGVGLVRGCGCKKVCYCK 57
 Db 1 MASVAGPISALVILALCTEPATQDCSAGQCAAEAPPCPNVSLVLCGCGCKVCYCK 60
 Oy 58 KOLWECSTQPCDHTKGLCECNQASSTALCKICRMOSEGRCEYNSRTYONCESFPNCK 119
 Db 61 KOLWECSTQPCDHTKGLCECNQASSTALCKICRMOSEGRCEYNSRTYONCESFPNCK 117
 Oy 118 KRCCTCIGAVGCIPLCPQELSLPMLGCPMPRLVKTGQCCCEWYCDDESIKDPMEDDGL 177
 Db 120 KYCTCIGAVGCIPLCPQELSLPMLGCPMPRLVKTGQCCCEWYCDDESIKDPMEDDGL 168
 Oy 178 LKGEGLDSEVELTFNNELAVKSSSLKRLVEGNEP-RILYNLQOCCTVOTTSMS 236
 Db 169 LKGEGLDSEVELTFNNELAVKSSSLKRLVEGNEP-RILYNLQOCCTVOTTSMS 205
 Oy 237 SOCSKTGCGISTRTVNDNPECLVKEERICVBPCCOPYSSLKAKKCKSKTKKSPPEVR 296
 Db 206 SOCSKTGCGISTRTVNDNPECLVKEERICVBPCCOPYSSLKAKKCKSKTKKSPPEVR 265
 Oy 297 FTYAGCISVYKRYKRCGSCVGRCCCPOLRTFYVMKRFCEDEGFPSKNYMIQSCCKV 356
 Db 266 FTYAGCISVYKRYKRCGSCVGRCCCPOLRTFYVMKRFCEDEGFPSKNYMIQSCCKV 325
 Oy 357 NCPHANEALAPFYRLFMIDHKRD 376
 Db 326 NCPHANEALAPFYRLFMIDHKRD 347

RESULT 4

connective tissue growth factor - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
 C:Accession: A40551, S44205A, J. Botter, R.L.; Grotendorst, G.R.
 Dev. Cell Biol. 11, 1285-1294, 1991
 A:Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human v
 A:Reference number: A40551, MUID:91373462, PMID:1654388
 A:Accession: A40551
 A:Molecule type: mRNA
 A:Residues: 1-349

 A:Cross-references: GB:M02931; GB:M05965; GB:S5201; NID:g180923; PIDN:AAA91279.1; PI
 submitted to the EMBL data library, April 1994
 A:Description: Differential cloning and expression of human connective tissue growth
 A:Reference number: S44205
 A:Accession: S44205
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-349 <DE>
 A:Cross-references: EMBL:X78947; NID:g474933; PID:g474934

Query Match 45.0%; Score 931; DB 2; Length 349;
 Best Local Similarity 46.9%; Pred. No. 1.3e-62;
 Matches 175; Conservative 57; Mismatches 101; Indels 40; Gaps 8;

9 LAIVYTLHTRALC-STCMAACGPTL-APKACGAYGVYGGGCCCKCAACANLNDKSC 66
 11 VAVVYTLALCSRAVAGNCKSGGCGCDPEAPNCPAGVSLVDDCCGCAACOLSELCTE 70
 67 TQCFDHTKGLCEVNGASSTALMGICRAQSEGRCEVNSITVNGSSSPCKNHCCTDGC 126
 71 RDCPCPKGLCPDPSRANIKYGVCAK-IDAACITGEGVIRSGSSSPCKVOCYCTDGC 129
 127 ANVCIPICPELSTPLNCGCNPRVYVGGCCCEPMVCKNHCCTDGC 126
 130 ANVCIPICSNVRLVSPCCPFPRVYVLPKCGCEVMDPEP-----KQ----- 172
 187 ASEVELTRNNELIANGKSSSLKRL-PVCGMEPRILVPLDQGCIVOTVTSMSQSKT 245
 173 -----TVGAPLAALRIEITGDPPTM-----RANCLVOTVTSMSQSKTGM 215
 246 GISTPVTNPNPEKRIEPIEYRCQGVYSSIKKCKGSKSTKSPPEVAFVACLS 305
 216 GISTPVTNPNNSCRLEKRSCLVYR/CADIDEMIKKKKCKRTKISKRIPELSCGTS 275
 306 VKKRYPCGSCVDGRCCTPOLVTVTKMRKREDETFEKKVMYLOSKCNKNYCNHAEVA 365
 276 MKTIRAFCCGCTDGRKCHETHTTLVVERKCPDSEVMAKNMFKTQCHNCIDNDI 335
 366 APPEY-RILPNDI 376
 336 FESLYEKRYGDM 348

RESULT 5
 520078
 NOV protein - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: 520078
 R:Joliot, V.; Martinier, C.; Dambrine, G.; Plassiat, G.; Brisac, M.; Crochet, J.; Perh
 Mol. Cell. Biol. 12, 10-21, 1992
 A:Title: Proteolipid rearrangements and overexpression of a new cellular gene (nov) in myel
 A:Accession: 520078
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-351 <JOL>
 A:Cross-References: EMBL:X59284; NID:963702; PIDD:CAA1975.1; PID:963703
 A:Genes: NOV

Query Match 40.4%; Score 855.5; DB 2; Length 351;
 Best Local Similarity 44.2%; Pred. No. 1.3e-55;
 Matches 165; Conservative 43; Mismatches 104; Indels 61; Gaps 8;

11 LVYTLHTRALS-----TCPAC--HCPLEAPKACGAYGVYGGGCCCKCAACOLNDC 64
 12 LVYTLHTRALS-----TCPAC--HCPLEAPKACGAYGVYGGGCCCKCAACOLNDC 71
 65 SKTQCDHRTKGLCEVNGASSTALMGICRAQSEGRCEVNSITVNGSSSPCKNHCCTDGC 124
 72 SPLTLCDESGALVCDRGPEGCGAGLCV-LBEDNCVCFGMRITRANGEPPOPCRYOCICR 130
 125 DGAAGCIPICPELSTPLNCGCNPRVYVGGCCCEPMVCKNHCCTDGC 180
 131 DQGLCPKMGKGLDLPDPCFFPRKILEYPOECCKMVC-----DPDEYV-LLDGFAM 182
 181 -----KEGLDPASEVELTRNNELIANGKSSSLKRLPVGMEPRILVPLDQGCIVOT 234
 183 AAVROEATLGIQVSD-----SSANCKDEPT 207
 235 SMSQSKTGGTGLSTRVTDNPECRILVEIRLICEVRCQGVYSSILKKKCKSKTSKSP 294

DB 208 EMSACSKCGSESTRTVYTNNOCEVYKOTLOMRCEKNEPSC-KKKGKIDOTKSKM 266
 295 PVAFYTAGLSVTKTRIPYCGSCYDRCCTPOLVTRVNRKREDETFEKKVMYLOSKCN 354
 267 AVAFYTKNTISVQTRFATDGLCHDRCCCTNNHTVTVLVEHRODGFATKAKMULNVCV 326
 355 CYNCPHANEAF 367
 327 CHONCPHMANAF 339

RESULT 6
 138063
 gene nov protein - human
 C:Species: Homo sapiens (man)
 C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 05-Nov-1999
 C:Accession: 138063
 R:Martinier, C.; Huff, V.; Joubert, I.; Badziak, M.; Saunders, G.; Strong, L.; Perh
 Oncogene 9, 2729-2732, 1994
 A:Title: Structural analysis of the human nov protein oncogene and expression in Wilms
 A:Accession: 138063
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-357 <RESS>
 A:Cross-References: EMBL:X78351; NID:9587422; PIDD:CAA55146.1; PID:9825696
 A:Genes: nov
 A:Accession: 138063
 C:Superfamily: thrombospondin type 1 repeat homology <THRI>
 F:203-250/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 39.5%; Score 834.5; DB 2; Length 357;
 Best Local Similarity 44.0%; Pred. No. 4.7e-54;
 Matches 160; Conservative 48; Mismatches 117; Indels 39; Gaps 8;

7 PALAVYTLHTRALST--CPAC--HCPLEAPKACGAYGVYGGGCCCKCAACOLNDC 62
 14 QCLCTFLHLHGVAAATQRPPGCFRCPCNPPFCAGVRAVYDGCSCGCVCAHNGE 73
 63 DSKTQCDHRTKGLCEVNGASSTALMGICRAQSEGRCEVNSITVNGSSSPCKNHCCT 122
 74 SCSDLEHDESSGALYCDMSADSHQGLCTA-VEEDNCVCFGMRITRANGEPPOPCRYOCICR 132
 123 CIDAVGCIPLCPRELSTPLNCGCNPRVYVGGCCCEPMVCKNHCCTDGC 182
 133 CRDQDQICVRCQDLYLLPEPNCAPRVEVEPCECKMVC-----EEDISGLT 185
 183 LCFDASEVELTRNNELIANGKSSSLKRLPVGMEPRILVPLDQGCIVOTVTSMSQSKT 242
 186 LA-AVIREATLVEY-----SSQSV-----NCLDITETKSKS 219
 243 CQGVSTRVTDNPECRILVEIRLICEVRCQGVYSSILKKKCKSKTSKSPPEVAFVACLS 301
 220 CGKGVSTRVNRNNOCEVYKOTLOMRCEKNEPSC-KKKGKIDOTKSKM 354
 302 GCLSVKRYPCGSCVDGRCCTPOLVTVTKMRKREDETFEKKVMYLOSKCNKNYCNHAEVA 365
 280 NCSLHTRFTRNGVCSHONCTNNHTVTDGAFRCSDQVYKRVYVTVOTCHNDC 339
 362 ANA 365
 340 NNEA 343

RESULT 7
 727283
 hypothetical protein Y640A.f - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: 727283
 R:Ainscough, R.

Hypothetical protein F40E10.4 - *Caenorhabditis elegans* (fragment)

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22025

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19503

A:Accession: T22025

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-601 <M11>

A:Sequence reference: EMBL:Z69792, P1DN:CAA93668.1, GSPDB:GN00028, CESP:F40E10.4

A:Experimental source: Clone F40E10

C:Genetics:

A:Gene: CESP:F40E10.4

A:Map position: X

Query Match 6.9%; Score 145; DB 2; Length 601;

Best Local Similarity 19.8%; Pred. No. 0.0034;

Matches 93; Conservative 52; Mismatches 142; Indels 182; Gaps 24;

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OY 30 CHPELEAKKACAVGLVNDGCG---CKYKAGLNEGCSMQPC-----70
Db 162 CDCPME-----YEKHCEDKLEYCTKRLN-PCENNGKCIPIGSSYSCMCSPGFT 209
OY 71 -----DHKGLGECNFGASSTALNGI-----CRAQSRGPCEYNSRI--YONGSEF 113
Db 210 GNNCETNIDCKNVEGCKONGGS--CYDILSTGCLCRPGTAQCYCTEPPMDMETQKTDNC 267
OY 114 QPMCKHO-----CTCIDAVGCIPLCPQELSLPLGCPNP-----148
Db 268 QQSACGSGSECVASONSIDFTCKGHGFSG--PSCDROMS--VGKRNFGAYALDPLASD 322
OY 149 -----ELVKYVGGCCCEWVCEDESIKOPMED 174
Db 323 GTTITLRTSKTIGLLTYGDDEYSNELYDGNALVYIIGTFPAHMTSSVKNVDLPH 382
OY 175 QDDLGRKE---LGFDAEVELTRN---NELAVGK-----203
Db 383 RIISFTSRKCFQIDKNPQVIVENSQSKDLYTKGEMLYIGLPIEKSQDAKRPRHYK 442
OY 204 -GSSLKRLPYPMPEPRILYN--PLQGKCIQVOTSMGCSKT-----CTGISTRYT 252
Db 443 NMSSLK-----GCISSTINMPVILQALLENVNEGSCANTVNFCAIDQNG---KCI 494
OY 253 ND--NPRCRLVETRICEPGCPGVYSLSKGGKCSKTSKSPKPEPFTAGCLSVKXR 310
Db 495 NNALSPKGYWCO---CDSHSGS---HCDKRIKCDKOKFRRHIE---NECRSVDRIK 544
OY 311 ---FRYSCGCDGCTCPDLIRIVKMKFRGEGGTSKMMVLIQSCIC 355
Db 545 IACNKGTOG--EONCTAVAKKOKHVMICKNGTTKISTVHIIRGCG 591

```

Search completed: July 8, 2003, 12:31:40

Job time : 43 secs

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Genome version 5.1.6
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OM protein - protein search, using SW model

Run on: July 8, 2003, 12:13:12 ; Search time 23 Seconds
(without alignments)
687,064 Million cell updates/sec

Title: US-09-901-910-2

Sequence: 1 MSRRARALATVTLILHLTR.....ANEAPFYRLFDNKHFRD 381

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 40% summaries

Database : SWISSPROT_40%*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	ID	Description
1	2115	100.0	381	1 CYRG_HUMAN	O00622 homo sapien
2	1938	97.6	379	1 CYRG_MOUSE	P18406 mus musculu
3	1938	97.6	379	1 CYRG_MOUSE	P18406 mus musculu
4	952.5	46.3	348	1 CTGF_MOUSE	P13336 gallus galli
5	951	45.0	349	1 CTGF_MOUSE	P29279 homo sapien
6	937	44.3	349	1 CTGF_BOVIN	O18179 bos taurus
7	910	43.0	349	1 CTGF_BOVIN	O18179 bos taurus
8	855.5	40.4	351	1 NOV_CHICK	P28686 gallus galli
9	852	40.3	352	1 NOV_CHICK	P47452 coturnix co
10	834.5	38.5	357	1 NOV_HUMAN	P51609 xenopus lae
11	823.5	38.2	343	1 NOV_HUMAN	P51609 xenopus lae
12	811	36.6	344	1 NOV_HUMAN	P51609 xenopus lae
13	159	7.5	1700	1 BAR3_CHICK	P98089 rattus norv
14	153	7.2	1178	1 TSP2_MOUSE	P35440 gallus galli
15	152.5	7.2	1178	1 TSP2_MOUSE	P35440 gallus galli
16	152	7.2	5376	1 ZAN_MOUSE	O08799 mus musculu
17	151	7.1	3110	1 LMA2_HUMAN	P24043 homo sapien
18	148.5	7.0	1282	1 ZAN_MOUSE	P24043 homo sapien
19	148.5	7.0	1282	1 ZAN_MOUSE	P24043 homo sapien
20	148.5	7.0	1282	1 ZAN_MOUSE	P24043 homo sapien
21	143	6.8	1173	1 TSP1_HUMAN	O02817 homo sapien
22	141	6.7	5179	1 TSP1_HUMAN	O02817 homo sapien
23	140.5	6.6	2703	1 NOTC2_MOUSE	P83110 homo sapien
24	138	6.5	453	1 HRA3_HUMAN	P04275 homo sapien
25	138	6.5	453	1 HRA3_HUMAN	P04275 homo sapien
26	137	6.5	2482	1 TSP1_MOUSE	O28633 sus scrofa
27	137	6.5	2482	1 TSP1_MOUSE	O28633 sus scrofa
28	137	6.5	1170	1 TSP1_MOUSE	O28633 sus scrofa
29	137	6.5	1170	1 TSP1_MOUSE	O28633 sus scrofa
30	136	6.4	2531	1 TSP1_MOUSE	O28633 sus scrofa
31	136	6.4	2531	1 TSP1_MOUSE	O28633 sus scrofa
32	135	6.4	4773	1 FPG_MOUSE	O28633 sus scrofa
33	135	6.4	1168	1 FPG_MOUSE	O28633 sus scrofa

34	134	6.3	1056	1 MUC5_HUMAN	P98088 homo sapien
35	134	6.3	1218	1 JAC1_MOUSE	O99400 mus musculu
36	134	6.3	2871	1 EBN1_HUMAN	P35555 homo sapien
37	133.5	6.3	1106	1 STC2_MOUSE	P40798 drosophila
38	133.5	6.3	1106	1 STC2_MOUSE	P40798 drosophila
39	133.5	6.3	1106	1 STC2_MOUSE	P40798 drosophila
40	133	6.3	1955	1 HRA3_MOUSE	P35441 mus musculu
41	133	6.3	1170	1 TSP1_MOUSE	P35441 mus musculu
42	133	6.3	2813	1 VWF_HUMAN	P04275 homo sapien
43	133	6.3	3106	1 LMA2_MOUSE	O60675 mus musculu
44	133	6.3	3672	1 LMA2_MOUSE	O60675 mus musculu
45	131.5	6.2	703	1 FBTL_HUMAN	P23142 homo sapien

ALIGNMENTS

RESULT 1	CYRG_HUMAN	STANDARD:	PROT:	381 AA.
ID	O00622	Q99400	Q99400	
DT	15-JUN-1998 (rel. 36)	15-JUN-1998 (rel. 36)	15-JUN-1998 (rel. 36)	
DE	15-JUN-2002 (rel. 41)	15-JUN-2002 (rel. 41)	15-JUN-2002 (rel. 41)	
DE	CYRG1 protein precursor (Cysteine-rich, angiogenic inducer, 61) (GIG1 protein) (Insulin-like growth factor-binding protein 10).			
GN	CYRG1 OR IGFBP10 OR GIG1			
OS	Homo sapiens (human)	Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
NC	NCBI_TaxID=9606;			
RA	SEQUENCE FROM N.A.			
RA	Albrecht C., von der Kammer H., Klaudiny J., Mayhaus M., Nitsch R.M.,			
RA	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RA	SEQUENCE FROM N.A.			
RA	MEDLINE=97260750; PubMed=9135077;			
RA	Jay P., Berge-LeFranc J.L., Marsotlier C., Mejean C., Taviaux S.,			
RA	Beta P.;			
RT	"The human growth factor-Inducible immediate early gene, CYRG1, maps			
RT	to chromosome 1p.;"			
RT	oncogene 14:1753-1757(1997).			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=96197344; PubMed=9536281;			
RP	Mahtoele C., Viegas-Pequignot E., Nguyen V.C., Perbal B.;			
RP	"Chromosomal mapping and expression of the human cyrg1 gene in tumor			
RP	cells from the nervous system.;"			
RP	Mol. Pathol. 50:310-316(1997).			
RP	SEQUENCE FROM N.A.			
RP	Medline=97260750; PubMed=9135077;			
RP	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RP	Kolesnikova T.V., Lau L.F.;			
RP	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RP	Bl.A.B., Yu L.;			
RP	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RP	Schuetz N., Lechner A., Groll C., Koehle J., Jakob F.;			
RP	"Regulation of nCR61 by vitamin D, serum and cytokines in fetal human			
RP	osteoblasts.;"			
RP	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RP	Leung E., Tai G., Estable M., Liu J., Chow C., Sawowski I.;			
RP	"Organization and expression of the CYRG1 gene in normal human			
RP	fibroblasts.;"			
RP	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
RP	(8)			
RP	SEQUENCE FROM N.A.			

CC TISSUE: Lung, Placenta, and Skin;
 CC SwissProt: P02201 (1997-2001) to the EMBL/GenBank/DBPJ databases.
 CC FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
 CC PROTEINS: PROMOTES PROLIFERATION, MIGRATION AND ADHESION (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY. CEF-10/CYR61/CTGF/ETSP-12/NOV PROTEIN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WVF DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y12084; CAW2802.1; -
 CC EMBL: U62015; AAB58319.1; -
 CC EMBL: Y11307; CAW2167.1; -
 CC EMBL: AF003594; AAB61240.1; -
 CC EMBL: AF031985; AAB84227.1; -
 CC EMBL: AF032860; CAB01986.1; -
 CC EMBL: AF032860; CAB01986.1; -
 CC EMBL: BC0011271; AAH01271.1; -
 CC EMBL: BC0091199; AAH09199.1; -
 CC EMBL: BC016952; AAH16952.1; -
 CC GenBank: HGNC:2654; CYR61.
 CC MIM: 602369; -
 CC InterPro: IPR003629; Cys_knot.
 CC InterPro: IPR003629; Cys_knot.
 CC InterPro: IPR000884; TSP1.
 CC InterPro: IPR001007; WVF.C.
 CC Pfam: PF000097; Tsp_1; 1.
 CC Pfam: PF000097; Tsp_1; 1.
 CC Pfam: PF000093; WVC; 1.
 CC Pfam: PF002139; IGFBP; 1.
 CC Pfam: PF002139; IGFBP; 1.
 CC SMART: SM00121; IB; 1.
 CC SMART: SM00121; IB; 1.
 CC SMART: SM00209; TSP1; 1.
 CC SMART: SM00214; WVC; 1.
 CC PROSITE: PS00222; IGF_BINDING; 1.
 CC PROSITE: PS01185; CTCK_1; 1.
 CC PROSITE: PS01225; CTCK_2; 1.
 CC PROSITE: PS01208; WVF.C; 1.
 CC KEGG: factor binding; signal.
 CC KEGG: factor binding; signal.
 CC KEGG: factor binding; signal.
 CC CHAIN 25 381
 CC DOMAIN 98 164 WVF.
 CC DISULFID 286 323 CTCK.
 CC DISULFID 303 337 BY SIMILARITY.
 CC DISULFID 314 352 BY SIMILARITY.
 CC DISULFID 322 359 BY SIMILARITY.
 CC CONFLICT 165 165 E -> Q (IN REF. 3).
 CC CONFLICT 210 210 L -> I (IN REF. 5).
 CC CONFLICT 220 220 L -> R (IN REF. 5).
 CC CONFLICT 369 369 F -> L (IN REF. 7).
 CC SEQUENCE 381 AA; 42026 MW; FCDSD39COT8CAQDI CMG64;
 CC -----
 CC Query Match 100 0%: Score 2115; DB 1; Length 381;
 CC Best Local Similarity 100 0%: Pctd No. 3; 3e-15;
 CC Matches 381: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 NCEDSKTQPCDHRTKGLCEPCGASSTALGICPAASGEPKCEVNSRITONGESFOPKCHD 120
 OY 121 CTGIDGAVCCIPICQELSLPACQCNRLRYVTGQCCEWCCDESTKOPREDOGILG 180
 DB 121 CTGIDGAVCCIPICQELSLPACQCNRLRYVTGQCCEWCCDESTKOPREDOGILG 180
 OY 181 KELGDSASVELTRNNELAVGKSSSLRPFQCEPRILYVNLQGKICVOTTSWQCS 240
 DB 181 KELGDSASVELTRNNELAVGKSSSLRPFQCEPRILYVNLQGKICVOTTSWQCS 240
 OY 241 KCTGCTSTRTNDPRLYKEMRLCVRPGQVSSLKQKCKTKKSSPEPRARY 300
 DB 241 KCTGCTSTRTNDPRLYKEMRLCVRPGQVSSLKQKCKTKKSSPEPRARY 300
 OY 301 AGCSLVKKRYKCYSCVDRCRCPDLPFRVYKMRCEDEGETSKNNWV10SKCNVCP 360
 DB 301 AGCSLVKKRYKCYSCVDRCRCPDLPFRVYKMRCEDEGETSKNNWV10SKCNVCP 360
 OY 361 HANEAPPPYELNDHKFRD 381
 DB 361 HANEAPPPYELNDHKFRD 381
 CC -----
 CC RESULT 2
 CC CYR61_MOUSE
 CC ID CYR61_MOUSE STANDARD; PRT; 379 AA.
 CC AC 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61)
 CC (insulin-like growth factor-binding protein 10) (3ch61).
 CC NM 006109 (GenBank)
 CC OR CYR61 OR IGFBP10.
 CC CC (Cytosolic)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC -----
 CC (1)
 CC RN
 CC RP
 CC SEQUENCE FROM N.A.
 CC STRAIN: BALB/c; TISSUE: Embryonic fibroblast;
 CC ORIGIN: F20714; C.Dbed=235916; L. Lau I.F.;
 CC *Expression of cyr61, a growth factor-inducible immediate-early
 CC gene*;
 CC Mol. Cell. Biol. 10:3569-3577(1990).
 CC (2)
 CC RN
 CC RP
 CC SEQUENCE FROM N.A.
 CC STRAIN: BALB/c; TISSUE: Embryonic fibroblast;
 CC ORIGIN: F20714; C.Dbed=235916; L. Lau I.F.;
 CC *Promoter function and structure of the growth factor-inducible
 CC immediate early gene cyr61*;
 CC Nucleic Acids Res. 19:3261-3267(1991).
 CC (3)
 CC RN
 CC RP
 CC FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
 CC PROTEINS: PROMOTES PROLIFERATION, MIGRATION AND ADHESION.
 CC -1- FUNCTION: PROMOTES PROLIFERATION, MIGRATION AND ADHESION. BRAIN
 CC AND OVARY: MODERATE IN HEART, UTERUS, AND SKELETAL MUSCLE, HIGHEST
 CC IN LONG.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1) IN
 CC NORMAL CELLS, AND AT A CONSTANT LEVEL IN RAPIDLY GROWING CELLS.
 CC -1- INDUCTION: BY GROWTH FACTORS.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY. CEF-10/CYR61/CTGF/ETSP-12/NOV PROTEIN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WVF DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.
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CC -----
CC EMBL: M32490; AAA37512.1;
CC EMBL: X56790; CAA40109.1;
CC EMBL: M35682; A35682.1;
CC EMBL: M35682; A35682.1;
CC DR Interpro: IPR000355; Cys_knot.
CC DR Interpro: IPR000867; Insl_gro_fac_pr.
CC DR Interpro: IPR001007; WVF_C.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR SMART: SM00209; TSP1; 1.
CC DR SMART: SM00214; WVC; 1.
CC DR PROSITE: PS00222; IGF_BINDING; 1.
CC DR PROSITE: PS01185; CTCK; 1; 1.
CC DR PROSITE: PS01225; CTCK; 2; 1.
CC DR PROSITE: PS01225; CTCK; 2; 1.
CC DR Growth factor binding; 24.
CC FT SIGNAL 24 Potential.
CC FT CHAIN 25 379 CTR61 PROTEIN.
CC FT DOMAIN 98 164 WVC.
CC FT DOMAIN 284 358 CTCK.
CC FT DISULFID 284 321 BY SIMILARITY.
CC FT DISULFID 312 353 BY SIMILARITY.
CC FT DISULFID 312 353 BY SIMILARITY.
CC FT DISULFID 315 353 BY SIMILARITY.
CC FT DISULFID 320 357 BY SIMILARITY.
CC SEQUENCE 379 AA; 41109 MW; FAEBS01456AEE9 CRC64;

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Query Match 91.6%; Score 1938; DB 1; Length 379;
Best Local Similarity 91.4%; Pred. No. 4, 5e-137;
Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2;

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QY 1 MSRRIRALAVYLLHTLRLALSTCPAACHCELPAPKAGVGLVHGCGCCCKVCAKOL 60
DB 1 MSSSTRFLAVAVYLLHTLRLALSTCPAACHCELPAPKAGVGLVHGCGCCCKVCAKOL 60
QY 61 NECSKTRPODHTKLECNQASSTALGICRANOSRPRCEYNSRTYONESPONCKHO 120
DB 61 NECSKTRPODHTKLECNQASSTALGICRANOSRPRCEYNSRTYONESPONCKHO 120
QY 121 CTCTGAVGCIPLCPQELSLPRLVAVYTGCCCEWYCDSDSIKIPMEDODLLG 180
DB 121 CTCTGAVGCIPLCPQELSLPRLVAVYTGCCCEWYCDSDSIKIPMEDODLLG 180
QY 121 CTCTGAVGCIPLCPQELSLPRLVAVYTGCCCEWYCDSDSIKIPMEDODLLG 180
DB 121 CTCTGAVGCIPLCPQELSLPRLVAVYTGCCCEWYCDSDSIKIPMEDODLLG 180
QY 181 KEAGDASDEVELTNNELLAVGKSSLRKLPVTEGPRILVPL--QDQKCIYVTTSMQ 238
DB 179 -LGLDASDEVELTNNELLAVGKSSLRKLPVTEGPRILVPL--QDQKCIYVTTSMQ 236
QY 239 CSTGCTGISTRTVYNDNEPCRLVKEPRICEVRCQAPVYSIKKGRKSKSTKKSPREVF 288
DB 239 CSTGCTGISTRTVYNDNEPCRLVKEPRICEVRCQAPVYSIKKGRKSKSTKKSPREVF 286
QY 297 CASSCGTISTRTVYNDNEPCRLVKEPRICEVRCQAPVYSIKKGRKSKSTKKSPREVF 296
DB 297 TYAGCLSLKXKRPVYTGCCYVDGKCTVYITVYKRRPRDEGTEFSKVMYMAIQSTCKNIN 358
QY 297 TYAGCLSLKXKRPVYTGCCYVDGKCTVYITVYKRRPRDEGTEFSKVMYMAIQSTCKNIN 356
DB 297 TYAGCLSLKXKRPVYTGCCYVDGKCTVYITVYKRRPRDEGTEFSKVMYMAIQSTCKNIN 356
QY 359 CPEANEAAPPFRPLFNDIHKFRD 381
DB 357 CPEANEAAPPFRPLFNDIHKFRD 379

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RESULT 3
CBLD_CHICK STANDARD; PRT; 375 AA.
AC 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

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DE CER-10 protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC [1] _taxid-9031;
RP SEQUENCE FROM N.A.
RP MEDLINE-69145206; PubMed-2537491;
RA Simons D.L., Levy D.B., Yarnom Y., Erikson R.L.;
RT "Identification of a photol ester-repressible v-src-inducible gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1178-1182(1989).
CC - FUNCTION: PROBABLY SECRETED REGULATORY PROTEIN.
CC - SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY. CER-10/CYR61/CTCK/FTSP-12/NOV PROTEIN SUPRIMING.
CC - SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.
CC - SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.
CC -----
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CC
CC EMBL: J04496; AAA4661.1;
CC EMBL: J04496; AAA4661.1;
CC DR Interpro: IPR000355; Cys_knot.
CC DR Interpro: IPR000867; Insl_gro_fac_pr.
CC DR Interpro: IPR000867; TSP1.
CC DR Interpro: IPR001007; WVF_C.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR SMART: SM00209; TSP1; 1.
CC DR SMART: SM00214; WVC; 1.
CC DR PROSITE: PS00222; IGF_BINDING; 1.
CC DR PROSITE: PS01185; CTCK; 1; 1.
CC DR PROSITE: PS01225; CTCK; 2; 1.
CC DR PROSITE: PS01225; CTCK; 2; 1.
CC DR Growth factor binding; signal.
CC FT SIGNAL 1 22
CC FT CHAIN 23 375 CER-10 PROTEIN.
CC FT DOMAIN 98 164 WVC.
CC FT DOMAIN 284 358 CTCK.
CC FT DISULFID 284 321 BY SIMILARITY.
CC FT DISULFID 312 353 BY SIMILARITY.
CC FT DISULFID 312 353 BY SIMILARITY.
CC FT DISULFID 315 353 BY SIMILARITY.
CC FT DISULFID 320 357 BY SIMILARITY.
CC SEQUENCE 375 AA; 40651 MW; 95F2D553ED35D5AB CRC64;

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Query Match 80.38; Score 1699; DB 1; Length 375;
Best Local Similarity 80.28%; Pred. No. 2, 5e-117;
Matches 312; Conservative 19; Mismatches 41; Indels 12; Gaps 7;

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QY 1 MSRRIRALAVYLLHTLRLALSTCPAACHCELPAPKAGVGLVHGCGCCCKVCAKOL 59
DB 1 MSSSTRFLAVAVYLLHTLRLALSTCPAACHCELPAPKAGVGLVHGCGCCCKVCAKOL 59
QY 60 INEDSKTRPODHTKLECNQASSTALGICRANOSRPRCEYNSRTYONESPONCKHO 119
DB 60 INEDSKTRPODHTKLECNQASSTALGICRANOSRPRCEYNSRTYONESPONCKHO 119
QY 120 CTCTGAVGCIPLCPQELSLPRLVAVYTGCCCEWYCDSDSIKIPMEDODLLG 179
DB 120 CTCTGAVGCIPLCPQELSLPRLVAVYTGCCCEWYCDSDSIKIPMEDODLLG 177

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RESULT 10
 NOV_HUMAN STANDARD: PRT, 357 AA.
 ID NO. 78351, 196865.
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NOV protein homolog precursor (NovH) (Nephroblastoma overexpressed gene protein).
 GN NOV.
 OS Homo sapiens (human)
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RK MEDLINE=94366229; PubMed=7520150;
 RA Strong L.C., Cephal B., Joubert I., Badtloch M., Saunders G.F.,
 RT Structural analysis of the human nov proto-oncogene and expression in Wilms tumor.
 RL Oncogene 9:2729-2732(1994).
 CC (2)
 RN SEQUENCE FROM N.A.
 RC TISSUE-Skin;
 RK PubMed=105117;
 RA Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: INCREASED EXPRESSION IN WILMS TUMOR OF THE STROMAL TYPE.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CER-10/CYR61/CTGF/ETSP-12/NOV PROTEIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.
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 CC
 DR EMBL: X78351; CAAS5146.1; JOINED.
 DR EMBL: X78352; CAAS5146.1; JOINED.
 DR EMBL: X78353; CAAS5146.1; JOINED.
 DR EMBL: X78354; CAAS5146.1; JOINED.
 DR EMBL: X78355; CAAS5146.1; JOINED.
 DR EMBL: BC015028; AAI15028.1;
 DR Genem: HGNC:7885; NOV.
 DR NIM: 164958;
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR000867; Ins1_gro_fac-pr.
 DR InterPro: IPR000864; TSP1.
 DR InterPro: IPR001007; WFC.
 DR Pfam: PF00090; tsp-1; 1.
 DR Pfam: PF00093; WFC; 1.
 DR Pfam: PF00219; IGEPF; 1.
 DR SMART: SM00041; CT; 1.
 DR SMART: SM00121; IB; 1.
 DR SMART: SM00209; TSP1; 1.
 DR SMART: SM00248; WFC; 1.
 DR PROSITE: PS00222; WFC-BINDING; 1.
 DR PROSITE: PS01185; CTCK-1; 1.
 DR PROSITE: PS01225; CTCK-2; 1.
 DR PROSITE: PS01208; WFC; 1.
 DR ProTo-oncogene: Growth factor binding; Signal.
 KW SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 357 NOV PROTEIN HOMOLOG.

FT DOMAIN 108 174 WFC.
 FT DOMAIN 264 338 CTCK.
 FT DISULFID 264 301 BY SIMILARITY.
 FT DISULFID 264 301 BY SIMILARITY.
 FT DISULFID 281 315 BY SIMILARITY.
 FT DISULFID 292 331 BY SIMILARITY.
 FT DISULFID 300 337 BY SIMILARITY.
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 97 97 N -> K (IN REF. 2).
 SO SEQUENCE 357 AA; 39162 MW; 035DBE4576B085B CRC64;
 Query: Match 36 5%; Score 834.5; DB: 1; Length 357;
 Best Local Similarity 44.0%; pred No. 3; e=55;
 Matches 160; Conservative 48; Mismatches 117; Indels 39; Gaps 8;
 QY 7 RALALVTLLHTRALST--CPAA--HCPILAKKAGVGLVRYGCGCCRYKAKLME 73
 DB 14 QCLCLRELLHLIDQVAATGRCPCGCGRCAPLPICAPAVLALGSCCLWAKRKE 72
 QY 63 DCGRYOCHTGYGCEGNASSALKTGRROSEGRYRNRYNONGSEFDPNKHOT 122
 DB 74 SCSLEPDESSGLYDRASSNQGTCTA-VEGDNCCVGVATVYSGSEFQSCFKOOT 132
 QY 123 CIGSAVGCTPLCPQELSLPNIACGPRLKVTGCGCEPWCDEDSIKPMEDQSLGKE 182
 DB 133 GGG 185
 QY 183 LGFNAEVEITLNNELLAVKSKSITKLTVCWERILLINPLQOGKIVOTMSNOSCT 242
 DB 186 LA-ATREPAVLGEV---SSSV-----NCIEDITEMTACNS 219
 QY 243 CGTGISTRYVNDPEGRLEKRIEIOEVRGQ--PYSSLSKKKCKSKSEPPRYETA 301
 DB 220 CGMESTRYVNNKNOCEMLKOTRLVRECSDEPDPODKKCKLTKSLKATIHQK 279
 QY 302 GCLSYKRYKRCQVCGVGRCPDLPYVWAFRCDEGFPFSKNNWIOSCKCNVCPH 361
 DB 280 NCTSLHYTKPRCCVSDGRCPHNTKTIQAFQSPQIVKRPVWVIGTCHTCKP 339
 QY 362 ANEA 365 111
 DB 340 NNEA 343 111
 RESULT 11
 NOV_XENLA STANDARD: PRT, 343 AA.
 ID NO. XENLA.
 AC P51609;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NOV protein homolog precursor (NovH).
 GN NOV.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96257227; PubMed=8666280;
 RA Ying Z., King M.L.;
 RT Isolation and characterization of nov, a Xenopus laevis ortholog of the chicken nov gene.
 RL Gene 124:240-248(1994).
 CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CER-10/CYR61/CTGF/ETSP-12/NOV PROTEIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.

ID	NOV_MOUSE	STANDARD:	PRT:	354 AA.
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Nov protein homolog precursor (Novb) (Mepitrolastoma overexpressed protein).			
OS	Nov			
OS	Mus musculus (mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID	10090:			
NCBI	(1)			
NCBI	SEQUENCE FROM N.A.			
RA	MEDLINE-96204003; PubMed-8622864;			
RA	Martiniere C., Chevalier G., Rauscher F.J. III, Perbal B.;			
RC	Regulation of nov by WT1: a potential role for nov in			
RC	neoprogenesis.			
RC	Oncogene 12:1479-1493(1996).			
RL	-1- GROWTH REGULATION (BY SIMILARITY)			
CC	-1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING			
CC	-1- PROTEIN FAMILY: CEF-10/CYB61/CTGF/FLIP-12/NOV PROTEIN SUPERFAMILY.			
CC	-1- SIMILARITY: COMAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.			
CC	-1- SIMILARITY: COMAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.			
CC	THIS SWISS-PROT ENTRY IS COPY-LEFT. IT IS PRODUCED THROUGH COLLABORATION			
CC	WITH THE EUROPEAN BIOINFORMATICS INSTITUTE, THERE ARE NO RESTRICTIONS ON ITS			
CC	USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY			
CC	MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL			
CC	ENTITIES REQUIRES A LICENSE AGREEMENT (SEE http://www.isdb.ch/announcement/).			
CC	OR SEND AN EMAIL TO license@isdb-sib.ch).			
EMBL:	X91663; CAA65457			
EMBL:	X92537; CAA70454.1			
EMBL:	X96585; CAA65404.1			
MGI:	MGI:109185; NOV.			
InterPro:	IPR000359; Cys_Knot.			
InterPro:	IPR000867; Ins1_910_fac_pt.			
InterPro:	IPR000884; TSP1.			
InterPro:	IPR001007; WFC_C.			
Pfam:	Pf00090; IBD_1007.1			
Pfam:	Pf00093; WFC_1			
Pfam:	Pf00219; IGFBP_1			
SMART:	SM00041; CT_1			
SMART:	SM00121; IB_1			
SMART:	SM00209; TSP1_1			
SMART:	SM00243; WFC_1			
PROSITE:	PS01242; CTCK_BINDING_1.			
PROSITE:	PS01185; CTCK_1.1			
PROSITE:	PS01225; CTCK_2.1			
PROSITE:	PS01208; WFC_1			
PROTO-oncogene:	Growth factor binding: Signal.			
SIGNAL	1	21		
CHAIN	1	354		
DOMAIN	102	168		
DOMAIN	261	353		
DOMAIN	325	353		
DISULFID	276	312		
DISULFID	289	338		
DISULFID	292	330		
DISULFID	297	334		
BY SIMILARITY.				
POTENTIAL.				
NOV PROTEIN HOMOLOG.				
PROTEIN HOMOLOG.				

[illegible]

Oy	53	-----CKVC-----	-----ANQJNDGSDTPODHI	72
Oy		479 IPPEEGEHEHREDKCKVCLEGGSGVIOKPKARGNLTCEBEYQIVYVADRDPKCK	538	
Oy	73	IKKQKPEE-----TGASSTALKICIRAOSEPR-----CEINSTIYONGSDT	115	
Dy		73 TSCGCKADPKKCAKARPSSLLGAEVYKSEBHYGCKPCVYSCVYKQVCEHNAETOPS	598	
Dy	539	ITSCGCKADPKKCAKARPSSLLGAEVYKSEBHYGCKPCVYSCVYKQVCEHNAETOPS	598	
Oy	116	NCKHQCOTCID-----GAVGC-----IPLCPOLSLPYLACPNP-RUYKTCQCEANVC	164	
Dy	599	NKQDCVCTSDMSNDSTOLNISTCHYV-C-----NISCSEFEVYVSGCKCKQCT	650	
Oy	165	EDSHDHPD-----OGLLCKREL-----PDAEVELTNNELIANGKSGI-KRLPYVCA	215	
Dy	651	KCHIKRPEQOYIILKRGELQKPNDRCTFSCWKI-----NQDL-----SASVNTCPD	701	
Oy	216	BERLYNPLDQKCIQVTSW-SQGSKITGCTISTFYVNNPECHLWETRIIDEVRC	273	
Dy	702	DP-----SDCVGSIITYMCKCKC-----HINR-----NTVCS	733	
Dy	274	O-PYHSLSAKCKGCKSTKPKSEPPVPAVACLSCKKRYKC-GSC-----	YD 319	
Dy	734	ALPYKEI-----SYNGC-----AKNSMNCVSGSGCFWYSANQDLD	773	
Oy	320	G-----RCCTQTQUTYKAKRRCDEGFTSKSWMMIOGCKC	355	
Dy	774	HGSCGCRREMTSVWVSLDPCDGSLSIYTHIESCLC	811	
RESULT 15				
ID	TS2P2	CHICK	STANDARD;	PRF: 1178 AA.
AC	P35440;			
DT	01-JUN-1994	(Rel. 29, Created)		
DT	01-JUN-1994	(Rel. 29, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
GN	THS2	OR TS2P2		
GN	THS2	OR TS2P2		
GN	Gallus gallus	(Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianine;			
OC	Gallus.			
OC	NCBI_TaxID=9031;			
RE	SEQUENCE FROM N.A.			
RE	MEDLINE=91217026; PubMed=2022631;			
RE	Lawler J., Duguetta M., Ferro P.;			
RT	"Cloning and sequencing of chicken thrombospondin *;			
RL	J. Biol. Chem. 266:8039-8043(1991).			
CC	- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND			
CC	CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,			
CC	THROMBIN AND OTHERS. DISULFIDE-LINKED.			
CC	- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.			
CC	- SIMILARITY: CONTAINS 1 WFC DOMAIN.			
CC	- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.			
CC	- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.			
CC	- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.			
CC	THIS SEQUENCE ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH COLLABORATION			
CC	BETWEEN THE EUROPEAN BIOINFORMATICS INSTITUTE, THERE ARE NO RESTRICTIONS ON ITS			
CC	USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY			
CC	MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL			
CC	ENTITIES REQUIRES A LICENSE AGREEMENT (See http://www.1ab-sib.ch/announce/			
CC	OR send an email to license@sib-sib.ch).			
CC	ENTRY: NC0053; 515437.1.			
CC	PIR: J3904; A3904.			
DR	HSP: P00740; 1EDM.			
DR	InterPro: IPR000561; EGF_1like.			
DR	InterPro: IPR001881; EGF_Ca.			
DR	InterPro: IPR001791; Lamlnn.G.			

DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR003129; TSPV.
 DR InterPro: IPR001007; WFC_C.
 DR InterPro: IPR003367; TSP_3.
 DR Pfam: PF00090; TSP_1.
 DR Pfam: PF00093; WFC_1.
 DR Pfam: PF02210; TSPN_1.
 DR Pfam: PF02412; TSP_3.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00209; TSPN_3.
 DR SMART: SM00210; TSPN_1.
 DR SMART: SM00211; TSPN_1.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01208; WFC; 1.
 DR PROSITE: PS01208; WFC; 1.
 DR Glycoprotein: Cell adhesion; Repeat;
 DR Glycylle domain; Signal.
 FT CHAIN 23 1178
 FT DOMAIN 2 232 POTENTIAL
 FT DOMAIN 324 381 THROMBOSIN-BINDING 2
 FT DOMAIN 387 438 HEPARIN-BINDING (POTENTIAL).
 FT DOMAIN 441 499 WFC.
 FT DOMAIN 500 553 TSP TYPE-1 1.
 FT DOMAIN 556 655 TSP TYPE-1 2.
 FT DOMAIN 654 698 TSP TYPE-1 3.
 FT DOMAIN 731 766 EGF-LIKE 1.
 FT DOMAIN 767 789 EGF-LIKE 2.
 FT DOMAIN 790 825 EGF-LIKE 3.
 FT DOMAIN 826 848 TSP TYPE-3 1.
 FT DOMAIN 849 886 TSP TYPE-3 2.
 FT DOMAIN 887 923 TSP TYPE-3 3.
 FT DOMAIN 924 952 TSP TYPE-3 4.
 FT DOMAIN 953 954 TSP TYPE-3 5.
 FT DOMAIN 955 1178 TSP TYPE-3 6.
 FT SITE 934 935 C-TERMINAL.
 FT DISULFID 559 570 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 564 580 BY SIMILARITY.
 FT DISULFID 583 594 BY SIMILARITY.
 FT DISULFID 595 606 BY SIMILARITY.
 FT DISULFID 607 618 BY SIMILARITY.
 FT DISULFID 628 652 BY SIMILARITY.
 FT DISULFID 658 671 BY SIMILARITY.
 FT DISULFID 665 684 BY SIMILARITY.
 FT DISULFID 686 697 BY SIMILARITY.
 FT CARBOHYD 157 157 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 244 244 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 313 317 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 590 590 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 716 716 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 1075 1075 N-LINKED (GLCNAc...) (POTENTIAL).
 FT SEQUENCE 1178 AA: 131816 MW: 1370244 ZC8717A2 CRC64;
 Query Match 7.28; Score 152.5; DR 3; Length 1178;
 Best Local Similarity 21.08; Pred No 0.00052;
 Matches 65; Conservative 33; Mismatches 102; Indels 83; Gaps 13;

OY 262 KETRICEVAPC-----GOPYTSLAKG 283
 DB 487 RETEKCEKAPCPNMQMSPWSPWMSACTYTCGGTIERHSLCLNSPEPOYGEKICVGDTRKH 546
 OY 284 KQSTYKSPPEVAFITAGCTSVKATIRK KQSCVGR-CTTP 325
 DB 547 DMCKR-HDP-----TQCLSNCPAPAECLNSYPDCSMSCGP 582

Search completed: July 8, 2003, 12:29:23
 Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2003, 12:22:57 ; Search time 80 Seconds

Title: US-09-901-910-2
Perfect score: 2115

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Maximum DB seq length: 20000000000

Maximum DB seq length: 20000000000

Maximum Match 100%
Listing first 45 summaries

Database : ..

- ```

5: * sp_archaea:*
6: * sp_bacteria:*
7: * sp_fungi:*
8: * sp_human:*
9: * sp_invertebrate:*
10: * sp_mammal:*
11: * sp_mhc:*
12: * sp_organelle:*
13: * sp_phage:*
14: * sp_plant:*
15: * sp_virus:*
16: * sp_vertebrate:*
17: * sp_unclassified:*
18: * sp_rvms:*
19: * sp_bacteriaph:*
20: * sp_archaeoph:*

```

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID     | Description        |
|------------|--------|-------------|--------|----|--------|--------------------|
| 1          | 1938   | 91.6        | 379    | 11 | Q95S72 | Q95S72 ratfus no   |
| 2          | 1937   | 91.6        | 379    | 11 | Q95M76 | Q95M76 ratfus no   |
| 3          | 1667.5 | 78.8        | 375    | 13 | Q95R53 | Q95R53 xenopus la  |
| 4          | 1356   | 45.5        | 334    | 4  | Q95D19 | Q95D19 homo sapien |
| 5          | 1356   | 45.5        | 347    | 11 | Q95M83 | Q95M83 ratfus no   |
| 6          | 957    | 45.5        | 347    | 11 | Q95M83 | Q95M83 ratfus no   |
| 7          | 956.5  | 45.2        | 348    | 11 | Q95220 | Q95220 xenopus la  |
| 8          | 942    | 44.5        | 343    | 11 | Q42607 | Q42607 xenopus la  |
| 9          | 934    | 44.2        | 344    | 13 | Q95P80 | Q95P80 gallus ga   |
| 10         | 920.5  | 43.5        | 347    | 13 | Q95P80 | Q95P80 xenopus la  |
| 11         | 882    | 41.7        | 345    | 6  | Q97765 | Q97765 sus scrofa  |
| 12         | 819.5  | 38.7        | 351    | 11 | Q95Z05 | Q95Z05 ratfus no   |
| 13         | 771    | 36.5        | 367    | 6  | Q95388 | Q95388 mus muscul  |
| 14         | 759    | 35.9        | 367    | 11 | Q54775 | Q54775 mus muscul  |
| 15         | 759    | 35.9        | 367    | 11 | Q95P90 | Q95P90 ratfus no   |
| 16         | 628.5  | 29.7        | 331    | 4  | Q95958 | Q95958 homo sapien |

|    |                                                                       |                                        |     |         |
|----|-----------------------------------------------------------------------|----------------------------------------|-----|---------|
|    | 95872                                                                 |                                        | PRT | 379 AA. |
| ID | Q9E5T2                                                                |                                        |     |         |
| AC | Q9E5T2                                                                | FREELIMINARY                           |     |         |
| CD | Q9E5T2                                                                |                                        |     |         |
| DT | 01-MAR-2001                                                           | (TRPMURREL_16, Created)                |     |         |
| DR | 01-MAR-2001                                                           | (TRPMURREL_16, Last sequence update)   |     |         |
| DT | 01-JUN-2002                                                           | (TRPMURREL_21, last annotation update) |     |         |
| DE | Cysteine-rich protein 6L                                              |                                        |     |         |
| GN | CYR61                                                                 |                                        |     |         |
| OS | Rattus norvegicus (Rat.)                                              |                                        |     |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                        |     |         |
| OX | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |                                        |     |         |
| CC | NCBI_TaxID=10116;                                                     |                                        |     |         |
| RN | [1]                                                                   |                                        |     |         |
| RP | SEQUENCE FROM N.A.                                                    |                                        |     |         |
| RC | TISSUE=LUNG;                                                          |                                        |     |         |
| EC | MEDLINE=10435857, PubMed=10852911.                                    |                                        |     |         |
| FT | Nucleic Acids Res.                                                    |                                        |     |         |
| RT | Nichols B., von Der Kammer H., Mayhaus M., Klaudiny J., Schweizer M,  |                                        |     |         |
| RL | J Biol. Chem. 275:28929-28936(2000).                                  |                                        |     |         |
| DR | EMBL: AF218568, AGLI4364.1; "                                         |                                        |     |         |
| DR | InterPro: IPR000359; Cys_knot.                                        |                                        |     |         |
| DR | InterPro: IPR000867; Ins1_gro_fac.Pf.                                 |                                        |     |         |
| DR | InterPro: IPR000884; TSP1                                             |                                        |     |         |
| DR | InterPro: IPR001007; WVF.C                                            |                                        |     |         |
| DR | Pfam: PF00007; Cys_knot.1                                             |                                        |     |         |
| DR | Pfam: PF00219; TGFBRP; 1                                              |                                        |     |         |
| DR | Pfam: PF00269; tse_L1; 1                                              |                                        |     |         |
| DR | SFAM: SF00089; tse_L1; 1                                              |                                        |     |         |
| DR | SMART: SMOO041; CT_1                                                  |                                        |     |         |
| DR | SMART: SMOO121; IR_1                                                  |                                        |     |         |
| DR | SMART: SMOO209; TSP1; 1                                               |                                        |     |         |
| DR | SMART: SMO0214; WVC; 1                                                |                                        |     |         |
| DR | PROSITE: PS01185; CTC_K; 1                                            |                                        |     |         |
| DR | PROSITE: PS01245; CTC_K; 2; 1                                         |                                        |     |         |
| DR | PROSITE: PS00222; IGF_BINDING; 1                                      |                                        |     |         |
| DR | PROSITE: PS01208; WVC; 1                                              |                                        |     |         |

## ALIGNMENTS

|    |        |      |      |           |                     |
|----|--------|------|------|-----------|---------------------|
| 17 | 6.15   | 29.1 | 35.4 | 0.95389   | 0.95389 homo sapien |
| 18 | 53.35  | 24.8 | 25.0 | 4.07676   | 07676 homo sapien   |
| 19 | 45.35  | 24.8 | 25.1 | 0.92054   | 09204 homo sapien   |
| 20 | 49.55  | 23.4 | 28.0 | 4.09635   | 09635 homo sapien   |
| 21 | 49.55  | 23.4 | 28.0 | 4.09635   | 09635 homo sapien   |
| 22 | 48.95  | 23.7 | 17.6 | 1.11111   | 09111 homo sapien   |
| 23 | 37.75  | 17.8 | 128  | 11.09620  | 09200 rattus norv   |
| 24 | 34.1   | 16.1 | 100  | 4.09016   | 09016 homo sapien   |
| 25 | 34.1   | 16.1 | 113  | 11.09214  | 09214 rattus norv   |
| 26 | 336    | 15.9 | 119  | 11.09206  | 09206 mus spicile   |
| 27 | 336    | 15.9 | 119  | 11.09129  | 09129 mus musculu   |
| 28 | 293    | 13.9 | 230  | 4.09067   | 09067 homo sapien   |
| 29 | 195    | 9.2  | 237  | 4.09067   | 09067 homo sapien   |
| 30 | 195    | 8.9  | 237  | 4.09067   | 09067 homo sapien   |
| 31 | 176    | 8.5  | 13   | 0.99621   | 09621 mus musculu   |
| 32 | 176    | 8.5  | 13   | 0.99621   | 09621 mus musculu   |
| 33 | 174    | 8.2  | 179  | 5.09060   | 09060 dirosophila   |
| 34 | 174    | 8.2  | 1045 | 5.08345   | 08345 caenorhabdi   |
| 35 | 174    | 8.2  | 1070 | 5.08347   | 08347 caenorhabdi   |
| 36 | 174    | 8.2  | 1111 | 5.09406   | 09406 caenorhabdi   |
| 37 | 171.5  | 8.1  | 1036 | 4.09401   | 09401 homo sapien   |
| 38 | 171    | 8.1  | 1064 | 5.09402   | 09402 caenorhabdi   |
| 39 | 171    | 8.1  | 1064 | 5.09446   | 09446 chironomus    |
| 40 | 150.78 | 8.0  | 158  | 6.09570   | 09570 mus musculu   |
| 41 | 164    | 7.8  | 158  | 6.09572   | 09572 mus musculu   |
| 42 | 162.5  | 7.7  | 792  | 13.09023  | 09023 gallus galli  |
| 43 | 162.5  | 7.7  | 1095 | 13.09084  | 09084 gallus galli  |
| 44 | 160.5  | 7.6  | 2104 | 5.02181   | 02181 caenorhabdi   |
| 45 | 150.5  | 7.6  | 2104 | 5.09694   | 09694 caenorhabdi   |
| 46 | 159.5  | 7.5  | 406  | 11.092513 | 092513 mus musculu  |





```

Db 61 04GELCTERDCCPPIKOLTCODSSPANKRIGVCTAK-DGACVCGSVYSGESRPSCK 119
 119 HOGCTIDGAVGCPICLOPELSIPMLGCPNRLVATYGGCCFPWNCDEDSIKDPMEDDGL 176
 120 YOCCTIDGAVGCVPCLSMDVRLRPPDCCPPRRVRLGKCCBEMVCDP----- 167
 179 LKRELGFDASEVELTRNNELIANGKSSLRK-PVCGMPRLIYLPLOGCKIVOTTSM 237
 168 -----KORVAGPALAAVRLIEDTGFDPPIWK-----RANCLVOTTSM 205
 238 QCSCTGCGTISTRTVNTNNEPCKRLVETPIEVRCCQVYVSLKFKGCKSTKSPRY 297
 205 ACSCTGCMGISTRTVNTNNEPCKRLVETPIEVRCCQVYVSLKFKGCKSTKSPRY 265
 298 PTYAGCLSVKKYRPNYVCGSVYDRCCTPOLRTYVKKRRPCEDEGTFKRVMMHIOGCKCN 357
 265 FELSGCTSVKTYRPFVCGVCDGSCCTPHHTTLPVFKCPDDEIFMKKMMFRTKTCACH 325
 358 NCPHANEAPPEY-RLFNDI 376
 326 NCPDNDJFESLYRKNYGM 346
 326 NCPDNDJFESLYRKNYGM 346

RESULT 6
09WS1 ID 09WS1 PRELIMINARY: PRT: 347 AA.
AC 09WS1:
DT 01-NOV-1999 (TREMblrel, 12, Created)
DT 01-NOV-1999 (TREMblrel, 12, Last sequence update)
DT 01-JUN-2002 (TREMblrel, 21, Last annotation update)
DE Connective tissue growth factor.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Sequence from N.A.
RT Rattus norvegicus Connective tissue growth factor.*;
RT Submitted (1999-11-12) EMBL/GenBank/DBJ databases.
DR EMBL: AB021068. RNA82125.1;
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR000867; Insl_gro_fac.pr.
DR InterPro: IPR000884; TSP1.
DR Pfam: PF00007; Cys_knot.1.
DR Pfam: PF00007; Cys_knot.1.
DR Pfam: PF00093; IGBB; 1.
DR Pfam: PF00093; Cvc.1.
DR Pfam: PF00093; Cvc.1.
DR SMART: SM00041; CT.1.
DR SMART: SM00121; IB.1.
DR SMART: SM00209; TSP1.1.
DR SMART: SM00214; WVC.1.
DR PROSITE: PS01185; CCKC.1.1.
DR PROSITE: PS01223; CCKC.2.1.
DR PROSITE: PS01223; CCKC.2.1.
DR PROSITE: PS01208; WVC; UNKNOWN.1.
SQ Sequence 347 AA; 37837 MW; 6A69511DE72F81C CCKC4;

Query Match 45.28; Score 957; DB 11; Length 347;
Best Local Similarity 46.56; Pred. NO. 8.26-84;
Matches 177; Conservative 57; Mismatches 107; Indels 40; Gaps 7;

1 MESSIRALALVYTLTAL-STCPAACHGPE-ARCAVCGVLYRGGCCCNCA 60
 119 HOGCTIDGAVGCPICLOPELSIPMLGCPNRLVATYGGCCFPWNCDEDSIKDPMEDDGL 176
 120 YOCCTIDGAVGCVPCLSMDVRLRPPDCCPPRRVRLGKCCBEMVCDP----- 167
 179 LKRELGFDASEVELTRNNELIANGKSSLRK-PVCGMPRLIYLPLOGCKIVOTTSM 237
 168 -----KORVAGPALAAVRLIEDTGFDPPIWK-----RANCLVOTTSM 205
 238 QCSCTGCGTISTRTVNTNNEPCKRLVETPIEVRCCQVYVSLKFKGCKSTKSPRY 297
 205 ACSCTGCMGISTRTVNTNNEPCKRLVETPIEVRCCQVYVSLKFKGCKSTKSPRY 265
 298 PTYAGCLSVKKYRPNYVCGSVYDRCCTPOLRTYVKKRRPCEDEGTFKRVMMHIOGCKCN 357
 265 FELSGCTSVKTYRPFVCGVCDGSCCTPHHTTLPVFKCPDDEIFMKKMMFRTKTCACH 325
 358 NCPHANEAPPEY-RLFNDI 376
 326 NCPDNDJFESLYRKNYGM 346
 326 NCPDNDJFESLYRKNYGM 346

RESULT 7
092200 ID 092200 PRELIMINARY: PRT: 348 AA.
AC 092200:
DT 01-DEC-2001 (TREMblrel, 19, Created)
DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel, 21, Last annotation update)
DE Connective tissue growth factor.
GN CTGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA Sequence from N.A.
RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006783; AAH06783.1; -.
DR MGI: MGI:95537; Ctgf.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR000867; Insl_gro_fac.pr.
DR InterPro: IPR000884; TSP1.
DR Pfam: PF00007; Cys_knot.1.
DR Pfam: PF00007; Cys_knot.1.
DR Pfam: PF00093; IGBB; 1.
DR Pfam: PF00093; Cvc.1.
DR PROSITE: PS01185; CCKC.1. UNKNOWN.1.
DR PROSITE: PS01223; CCKC.2.1.
DR PROSITE: PS01223; CCKC.2.1.
DR PROSITE: PS01208; WVC; UNKNOWN.1.
SQ Sequence 348 AA; 37794 MW; 4D7B6D9089174049 CCKC4;

Query Match 45.28; Score 956.5; DB 11; Length 348;
Best Local Similarity 46.94; Pred. NO. 9.26-84;
Matches 179; Conservative 56; Mismatches 106; Indels 41; Gaps 8;

1 MESSIRALALVYTLTAL-STCPAACHGPE-ARCAVCGVLYRGGCCCNCA 57
 119 HOGCTIDGAVGCPICLOPELSIPMLGCPNRLVATYGGCCFPWNCDEDSIKDPMEDDGL 176
 120 YOCCTIDGAVGCVPCLSMDVRLRPPDCCPPRRVRLGKCCBEMVCDP----- 168
 178 LKRELGFDASEVELTRNNELIANGKSSLRK-PVCGMPRLIYLPLOGCKIVOTTSM 236
 169 -----KORVAGPALAAVRLIEDTGFDPPIWK-----RANCLVOTTSM 205

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[illegible][illegible]

|                   |                                                                  |                                                             |              |
|-------------------|------------------------------------------------------------------|-------------------------------------------------------------|--------------|
| QY                | 30                                                               | VKKRKKKSCGSDCDDCCPOLPRTVYKMKRRPEEDGCTSKNNVMYKSCAKYVNCNHNZ   | 369          |
| Db                | 271                                                              | VATTKRKKKSCGSDCDDCCPOLPRTVYKMKRRPEEDGCTSKNNVMYKSCAKYVNCNHNZ | 330          |
| OY                | 366                                                              | APPY--RLNPD 376                                             |              |
| Db                | 331                                                              | PESTLYRKMVGDM 343                                           |              |
| RESULT 10         |                                                                  |                                                             |              |
| 1                 | REFSEQ                                                           |                                                             |              |
| 2                 | APPRO                                                            | PRELIMINARY:                                                | PRT: 347 AA. |
| AC                | 09PT80:                                                          |                                                             |              |
| DT                | 01-MAY-2000 (TEMBLrel.13, Created)                               |                                                             |              |
| DT                | 01-MAY-2000 (TEMBLrel.13, Last sequence update)                  |                                                             |              |
| DT                | 01-JUN-2002 (TEMBLrel.21, Last annotation update)                |                                                             |              |
| DE                | Connective tissue growth factor.                                 |                                                             |              |
| DN                | CTGF                                                             |                                                             |              |
| ON                | Connective tissue growth factor.                                 |                                                             |              |
| OR                | Connective tissue growth factor.                                 |                                                             |              |
| OC                | Connective tissue growth factor.                                 |                                                             |              |
| OC                | Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae.      |                                                             |              |
| OC                | Notophthalmus.                                                   |                                                             |              |
| NCBI_TextId:8316; |                                                                  |                                                             |              |
| FN                | (1)                                                              |                                                             |              |
| RP                | SEQUENCE FROM N.A.                                               |                                                             |              |
| RP                | TISSUE=FORELIMB BLASTEM:                                         |                                                             |              |
| RP                | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.          |                                                             |              |
| RP                | 121                                                              |                                                             |              |
| RP                | SEQUENCE FROM N.A.                                               |                                                             |              |
| RC                | TISSUE=FORELIMB BLASTEM;                                         |                                                             |              |
| RC                | MEDLINE=9003008; PubMed=981373;                                  |                                                             |              |
| RC                | Cash D.E., Gates P.B., Imokawa Y., Brookes J.P.;                 |                                                             |              |
| RA                | Regulation of new connective tissue growth factor as a target of |                                                             |              |
| RA                | retinoid action in limb blastema cells.                          |                                                             |              |
| RL                | Gene 222,119-124,139(81) limb blastema cells.                    |                                                             |              |
| RL                | EMBL: AJ271167; C685965.1; -                                     |                                                             |              |
| DR                | Interpro: IPRO00359; Cys_knot.                                   |                                                             |              |
| DR                | Interpro: IPRO00867; Ins1_gro_fac.pr.                            |                                                             |              |
| DR                | Interpro: IPRO01007; WFC.                                        |                                                             |              |
| DR                | Interpro: IPRO00884; TSP1.                                       |                                                             |              |
| DR                | Pfam: PF00019; IGFBP1; 1.                                        |                                                             |              |
| DR                | Pfam: PF00090; TSP.1; 1.                                         |                                                             |              |
| DR                | Pfam: PF00093; WFC.1.                                            |                                                             |              |
| DR                | SMART: SM00121; CT; 1.                                           |                                                             |              |
| DR                | SMART: SM00121; IB; 1.                                           |                                                             |              |
| DR                | SMART: SM0209; TSP1; 1.                                          |                                                             |              |
| DR                | SMART: SM01185; WFC; 1.                                          |                                                             |              |
| DR                | PROSITE: PS01225; CTCK.2; 1.                                     |                                                             |              |
| DR                | PROSITE: PS02221; IGF_BINDING.1.                                 |                                                             |              |
| DR                | PROSITE: PS01208; WFC; UNKNOWN.1.                                |                                                             |              |
| SO                | SEQUENCE 347 AA: 38098 MW: 387E239927672C1 CRC64:                |                                                             |              |
| Query Match       |                                                                  |                                                             |              |
| 1                 | Meat Local Similarity                                            | 43.58; Score 920.5; DB 13; Length 347;                      |              |
| Matches           | 172; Conservative                                                | 46; Mismatches 107; Ids 51; Gaps 6                          |              |
| OY                | 9                                                                | LALVYVLLHLTRALSTCPACRCHLEAPKAPGVILRQCGCCYKAKMLKEGCKRQ       | 68           |
| Db                | 12                                                               | LILVALLVLSVSCA-QCGSGCRGCRNRPFCPCAGTSLVMVCGCCYKAKMLDEICETD   | 70           |
| OY                | 69                                                               | PCDHITGLGECNRGASSTALKGICRMOSEBRPCEYSNRITYESRFPNCKHCTGTGAV   | 128          |
| Db                | 71                                                               | VQDRHGLDPCGDSNKKRKTICAK-DNRFCVCGANTHSGSTSSCKIQCETLDDG       | 129          |
| OY                | 129                                                              | GCIPFLCPPELSLNLGCPNPRLVYKATGSCCEMYCDEDSIKOPMEDDGLGKELGPDAS  | 188          |
| Db                | 130                                                              | GCYVLCGVADVRLPSPDCEPFRKYLQSKCEBMYCQCR                       | 168          |
| OY                | 189                                                              | EVELTNNELLAV-----GKSSLRRLPYVCKMERPLTLNPLQGGKCTVOTSSQSK      | 241          |

|                       |                                                                      |               |                                                             |                                                         |             |        |       |                |     |
|-----------------------|----------------------------------------------------------------------|---------------|-------------------------------------------------------------|---------------------------------------------------------|-------------|--------|-------|----------------|-----|
| D6                    |                                                                      | 169           | --                                                          | EQFVGAALAMVROEYVEGPSSIMK                                | ---         | ----   | ----- | ANCIYOTEMSKCSK | 209 |
| Oy                    |                                                                      | 242           | TCTGGT                                                      | GTRATYNINNEBRIJVERICCEVRPCGQPVYSLLKKKKCKSRTKPKSPBAFFETA |             |        |       |                |     |
| D6                    |                                                                      | 210           | CGTGAGGATRYNYNKNRKEIKQSCLLNNYKCCDADENLKGNKCINFRKSLSPVKETKS  | 269                                                     |             |        |       |                |     |
| Oy                    |                                                                      | 302           | GCGLGVAKRRYKAYNGKRCRCPDRTPRYKKRPREGCEGSCWKMYIGOSCKYCNCHP    | 361                                                     |             |        |       |                |     |
| D6                    |                                                                      | 270           | GCTSVTKTYRAKPGCGCTDCRCCTPRATVTLPEVKCPCDEVMKKHMFYIKTCACHYNCG | 329                                                     |             |        |       |                |     |
| Oy                    |                                                                      | 362           | ANEAAAPFY--RLFNDI                                           | 376                                                     |             |        |       |                |     |
| D6                    |                                                                      | 330           | DMDIFSRATRKATIODA                                           | 346                                                     |             |        |       |                |     |
| RESULT                | 11                                                                   |               |                                                             |                                                         |             |        |       |                |     |
| ID                    | 097765                                                               |               | PRELIMINARY;                                                | PTT;                                                    | 349 AA.     |        |       |                |     |
| AC                    | 097765:                                                              |               |                                                             |                                                         |             |        |       |                |     |
| DT                    | 01-JUN-1999                                                          | (TEMPREL. 10, |                                                             |                                                         |             |        |       |                |     |
| DT                    | 01-JUN-2002                                                          | (TEMPREL. 21, |                                                             |                                                         |             |        |       |                |     |
| DE                    |                                                                      |               | Connective tissue growth factor.                            |                                                         |             |        |       |                |     |
| GN                    | CTGF.                                                                |               |                                                             |                                                         |             |        |       |                |     |
| OC                    | Sus scrofa (Pig).                                                    |               |                                                             |                                                         |             |        |       |                |     |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |               |                                                             |                                                         |             |        |       |                |     |
| OC                    | Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.                    |               |                                                             |                                                         |             |        |       |                |     |
| RN                    | [1]                                                                  | _TaxId=9823;  |                                                             |                                                         |             |        |       |                |     |
| RP                    | SEQUENCE FROM N.A.                                                   |               |                                                             |                                                         |             |        |       |                |     |
| RA                    | TISSUE=UTERUS;                                                       |               |                                                             |                                                         |             |        |       |                |     |
| RC                    | Handling P.A., Brigstock D.R.;                                       |               |                                                             |                                                         |             |        |       |                |     |
| FT                    | "Cloning and sequencing of a porcine connective tissue growth factor |               |                                                             |                                                         |             |        |       |                |     |
| RE                    | (CTGF) cDNA." 1995. to the EMBL/GenBank/DBJ databases.               |               |                                                             |                                                         |             |        |       |                |     |
| DL                    | Submitter (Seq. ID# 1995)                                            |               |                                                             |                                                         |             |        |       |                |     |
| DL                    | Submitter (Accession #)                                              |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | InterPro: IPR000867; Insl_gro_fac.pr.                                |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | InterPro: IPR000884; TSP1.                                           |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | InterPro: IPR001007; Cys_knot_1.                                     |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | Pfam: PF00007; Cys_knot_1.                                           |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | Pfam: PF00219; IGFBP_1.                                              |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | Pfam: PF00093; vsp_L1.                                               |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | SMART: SMART0121; IB_1.                                              |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | SMART: SMART0209; TSP1_1.                                            |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | SMART: SMART0214; WVC_1.                                             |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | PROSITE: PS01185; CTCK_1.                                            |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | PROSITE: PS01223; CTCK-LING_1.                                       |               |                                                             |                                                         |             |        |       |                |     |
| DR                    | PROSITE: PS01208; WVC_1.                                             |               |                                                             |                                                         |             |        |       |                |     |
| SO                    | SEQUENCE                                                             | 349 AA;       | 37946 MW;                                                   | 35BAB275AC1AB3A                                         | CRC64;      |        |       |                |     |
| Query Match           |                                                                      | 41.7%         | Score 882;                                                  | DB 6;                                                   | Length 349; |        |       |                |     |
| Best Local Similarity |                                                                      | 43.5%;        | Frag. No. 13;-76;                                           |                                                         |             |        |       |                |     |
| Matches               | 162;                                                                 | Conservative  | 59;                                                         | Mismatches                                              | 111;        | Indels | 40;   | Gaps           | 7   |
| Oy                    |                                                                      | 10            | AATVATLTATLRAL-STCAACACGCL-EAPKACAGAGLVNDGCGCYCAVOLANDRSMT  | 67                                                      |             |        |       |                |     |
| D6                    |                                                                      | 12            | AFVLLIALCSHPASQDQCSCCAAKKRAPGVSLLTEGCGCGLAHNRGLQLTER        | 71                                                      |             |        |       |                |     |
| Oy                    |                                                                      | 68            | GPCQHNLKLCNTNGASSTLTALMGCSSEBRCEYSMTITONGESCOPMKHCQTCDIA    | 130                                                     |             |        |       |                |     |
| D6                    |                                                                      | 72            | ACCPHKPLCLCDGSGPANRKLGVGAR-DCAFCVFGCVTVRGSGRSSCKIVCTQCLDA   | 137                                                     |             |        |       |                |     |
| Oy                    |                                                                      | 128           | VGTCPICAGSELSTPLGCRNPGRILNVYGCCCEMNOEDDSINDPDGDGLKLSLPFA    | 187                                                     |             |        |       |                |     |
| D6                    |                                                                      | 131           | VGCVPICSMOVRTPPCPPEPRRVYLKGCCCEMVQDDP-                      | 169                                                     |             |        |       |                |     |
| Oy                    |                                                                      | 188           | SEVELRNRMNELLANGKSSMLKR-PVGEDEPIILVYPLODGCKIVOTTSMGSCSNTGTS | 246                                                     |             |        |       |                |     |
| D6                    |                                                                      | 170           | -----KHVVGPRLALAIIRLEDTGGDPPTMM-----RANCIVOTTSMGSCSNTGSG    | 216                                                     |             |        |       |                |     |



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Oy 55 VQANQMEDSKTQPCDHRTKGLSECNF--GASSTALKGICMAOSEGRPCENSRITYONGSEF 113
Db 78 KCAQGLDNCETAAICDHRTGLSDSPRYAIGVC-AQVYGVCTLDGYRINQSGS 136
Oy 114 GPNCKKCTCIDGAVCTPLCDPELSPLNLCGPNPRLKYVGGCCGEMVCDSDS1KDPM 173
Db 137 GPNCKKCTCIDGAVCTPLC-LRYPRLMCPHRRYS1GECCEGVCMDA-KRRKR 194
Oy 174 DDDGLAKELGADPA-SEVELTRNNELINAVKSSLRLPVPGMEPRILYNLQGCITVO 232
Db 195 TAPRDGTT--ATDNGEIVAMHN-----CLAY 219
Oy 223 TTSNCSGTCGTGISTRVYNDNPECRILYKCEVPRGCPGVYSSLKKKCKSKTKS 292
Db 220 TSPMSCTSGTGGISTRISVNAVRCMPDESRCLMPCDDVDTIHLAKKCLAYGPE 279
Oy 293 PEVRFYTAGLSVAKIRPKYKCGSVQGRCTPOLRTFYVMKRFCEGDFTSKNVMAIOSK 352
Db 280 EASNTITLACGISTSYOKKCYGACDNRCCIPYKSKTISVDPGPGCSHQYLIANCF 339
Oy 340 CFCMLSCRNPD-----IPADLSYPD 361
RESULT 14
ID 054775 PRELIMINARY: PRT: 367 AA.
AC 054775:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI:Taxid=10090;
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